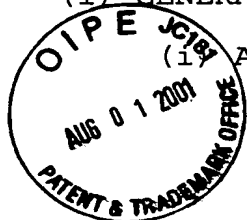


SEQUENCE LISTING

(1) GENERAL INFORMATION:



(i) APPLICANT: PAUL, PREM S.  
MENG, XIANG-JIN  
HALBUR, PATRICK G.  
MOROZOV, IGOR  
LUM, MELISSA A.

#6

(ii) TITLE OF INVENTION: A POLYNUCLEIC ACID ISOLATED FROM A PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), A PROTEIN ENCODED BY THE POLYNUCLEIC ACID, A VACCINE PREPARED FROM OR CONTAINING THE POLYNUCLEIC ACID OR PROTEIN,

(iii) NUMBER OF SEQUENCES: 77

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, P.C.  
(B) STREET: 1755 S. Jefferson Davis Highway, Suite 400  
(C) CITY: Arlington  
(D) STATE: Virginia  
(E) COUNTRY: U.S.A.  
(F) ZIP: 22202

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/131,625  
(B) FILING DATE: 05-OCT-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lavalleye, Jean-Paul M.P.  
(B) REGISTRATION NUMBER: 31,451  
(C) REFERENCE/DOCKET NUMBER: 4625-021-55X CIP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 413-3000  
(B) TELEFAX: (703) 413-2220  
(C) TELEX: 248855 OPAT UR

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGCCGTGTG GTTCTCGCCA AT

22

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCATTTCC CTCTAGCGAC TG

22

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGCGGAAC CATCAAGCAC

20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAACTTGACG CTATGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGTCTGGA TTGACGACAG

20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACTGCTAGG GCTTCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCATTCAGC TCACATAGCG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCGTCAAGT ATGGCCGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCATTCGCC TGACTGTCA

19

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGACGAGGA CTTCGGCTG

19

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTCTACCTG CAATTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGTATAGGA CCGGCAACCG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|  |      |
|--|------|
| GGCAGGCTTT GCTGTCCTCC AAGACATCAG TTGCCTTAGG CATCGCAACT CGGCCTCTGA  | 60   |
| GGCGATTTCG AAAGTCCCTC AGTGCCGCAC GGCGATAGGG ACACCCGTGT ATATCACTGT  | 120  |
| CACAGCCAAT GTTACCGATG AGAATTATTT GCATTCTCTCT GATCTTCTCA TGCTTTCTTC | 180  |
| TTGCCTTTTC TATGCTTCTG AGATGAGTGA AAAGGGATTT AAGGTGGTAT TTGGCAATGT  | 240  |
| GTCAGGCATC GTGGCAGTGT GCGTCAACTT CACCAGTTAC GTCCAACATG TCAAGGAATT  | 300  |
| TACCCAACGT TCCTTGGTAG TTGACCATGT GCGGCTGCTC CATTTCATGA CGCCCGAGAC  | 360  |
| CATGAGGTGG GCAACTGTTT TAGCCTGTCT TTTTGGCATT CTGTTGGCAA TTTGAATGTT  | 420  |
| TAAGTATGTT GGGGAAATGC TTGACCGCGG GCTGTTGCTC GCAATTGCTT TTTTGTGGT   | 480  |
| GTATCGTGCC GTCTTGTTTT GTTGCGCTCG TCAGCGCCAA CGGGAACAGC GGCTCAAATT  | 540  |
| TACAGCTGAT TTACAACCTG ACGCTATGTG AGCTGAATGG CACAGATTGG CTAGCTAATA  | 600  |
| AATTTGACTG GGCAGTGGAG TGTTTTGTCA TTTTTCCTGT GTTGACTCAC ATTGTCTCTT  | 660  |
| ATGGTGCCCT CACTACTAGC CATTTCCTTG ACACAGTCGG TCTGGTCACT GTGTCTACCG  | 720  |
| CTGGGTTTGT TCACGGGCGG TATGTTCTGA GTAGCATGTA CGCGGTCTGT GCCCTGGCTG  | 780  |
| CGTTGATTTG CTTCGTCATT AGGCTTGCGA AGAATTGCAT GTCCTGGCGC TACTCATGTA  | 840  |
| CCAGATATAC CAACTTTCTT CTGGACACTA AGGGCAGACT CTATCGTTGG CGGTCGCCTG  | 900  |
| TCATCATAGA GAAAAGGGGC AAAGTTGAGG TCGAAGGTCA CCTGATCGAC CTCAAAGAG   | 960  |
| TTGTGCTTGA TGGTTCCGCG GCTACCCCTG TAACCAGAGT TTCAGCGGAA CAATGGAGTC  | 1020 |
| GTCCTTAGAT GACTTCTGTC ATGATAGCAC GGCTCCACAA AAGGTGCTCT TGGCGTTTTT  | 1080 |
| TATTACCTAC ACGCCAGTGA TGATATATGC CCTAAAGGTG AGTCGCGGCC GACTGCTAGG  | 1140 |
| GCTTCTGCAC CTTTTGGTCT TCCTGAATTG TGCTTTCACC TTCGGGTACA TGACATTCGT  | 1200 |
| GCACTTTCAG AGTACAAATA AGGTCGCGCT CACTATGGGA GCAGTAGTTG CACTCCTTTG  | 1260 |
| GGGGGTGTAC TCAGCCATAG AAACCTGGAA ATTCATCACC TCCAGATGCC GTTTGTGCTT  | 1320 |

|            |             |             |            |            |            |      |
|------------|-------------|-------------|------------|------------|------------|------|
| GCTAGGCCGC | AAGTACATTC  | TGGCCCCCTGC | CCACCACGTT | GAAAGTGCCG | CAGGCTTTCA | 1380 |
| TCCGATTGCG | GCAAAATGATA | ACCACGCATT  | TGTCGTCCGG | CGTCCCGGCT | CCACTACGGT | 1440 |
| CAACGGCACA | TTGGTGCCCG  | GGTTAAAAAG  | CCTCGTGTTG | GGTGGCAGAA | AAGCTGTTAA | 1500 |
| ACAGGGAGTG | GTAAACCTTG  | TTAAATATGC  | CAAATAACAC | CGGCAAGCAG | CAGAAGAGAA | 1560 |
| AGAAGGGGGA | TGGCCAGCCA  | GTCAATCAGC  | TGTGCCAGAT | GCTGGGTAAG | ATCATCGCTC | 1620 |
| ACCAAAACCA | GTCCAGAGGC  | AAGGGACCGG  | GAAAGAAAAA | TAAGAAGAAA | AACCCGGAGA | 1680 |
| AGCCCCATTT | CCCTCTAGCG  | ACTGAAGATG  | ATGTCAGACA | TCACTTTACC | CCTAGTGAGC | 1740 |
| GTCAATTGTG | TCTGTCGTCA  | ATCCAGACCG  | CCTTTAATCA | AGGCGCTGGG | ACTTGCACCC | 1800 |
| TGTCAGATTC | AGGGAGGATA  | AGTTACACTG  | TGGAGTTTAG | TTTGCCTACG | CATCATACTG | 1860 |
| TGCGCCTGAT | CCGCGTCACA  | GCATCACCCT  | CAGCATGATG | GGCTGGCATT | CTTGAGGCAT | 1920 |
| CCCAGTGTTT | GAATTGGAAG  | AATGCGTGGT  | GAATGGCACT | GATTGACATT | GTGCCTCTAA | 1980 |
| GTCACCTATT | CAATTAGGGC  | GACCGTGTGG  | GGGTAAGATT | TAATTGGCGA | GAACCACACG | 2040 |
| GCCGAAATTA | AAAAAAAAAA  | AA          |            |            |            | 2062 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus  
(B) STRAIN: Iowa  
(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG TTG GGG AAA TGC TTG ACC GCG GGC TGT TGC TCG CAA TTG CTT TTT 48  
Met Leu Gly Lys Cys Leu Thr Ala Gly Cys Cys Ser Gln Leu Leu Phe  
1 5 10 15

|   |     |
|---|-----|
| TTG TGG TGT ATC GTG CCG TCT TGT TTT GTT GCG CTC GTC AGC GCC AAC | 96  |
| Leu Trp Cys Ile Val Pro Ser Cys Phe Val Ala Leu Val Ser Ala Asn |     |
| 20 25 30  |     |
| GGG AAC AGC GGC TCA AAT TTA CAG CTG ATT TAC AAC TTG ACG CTA TGT | 144 |
| Gly Asn Ser Gly Ser Asn Leu Gln Leu Ile Tyr Asn Leu Thr Leu Cys |     |
| 35 40 45  |     |
| GAG CTG AAT GGC ACA GAT TGG CTA GCT AAT AAA TTT GAC TGG GCA GTG | 192 |
| Glu Leu Asn Gly Thr Asp Trp Leu Ala Asn Lys Phe Asp Trp Ala Val |     |
| 50 55 60  |     |
| GAG TGT TTT GTC ATT TTT CCT GTG TTG ACT CAC ATT GTC TCT TAT GGT | 240 |
| Glu Cys Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly |     |
| 65 70 75 80   |     |
| GCC CTC ACT ACT AGC CAT TTC CTT GAC ACA GTC GGT CTG GTC ACT GTG | 288 |
| Ala Leu Thr Thr Ser His Phe Leu Asp Thr Val Gly Leu Val Thr Val |     |
| 85 90 95  |     |
| TCT ACC GCT GGG TTT GTT CAC GGG CGG TAT GTT CTG AGT AGC ATG TAC | 336 |
| Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Met Tyr |     |
| 100 105 110   |     |
| GCG GTC TGT GCC CTG GCT GCG TTG ATT TGC TTC GTC ATT AGG CTT GCG | 384 |
| Ala Val Cys Ala Leu Ala Ala Leu Ile Cys Phe Val Ile Arg Leu Ala |     |
| 115 120 125   |     |
| AAG AAT TGC ATG TCC TGG CGC TAC TCA TGT ACC AGA TAT ACC AAC TTT | 432 |
| Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe |     |
| 130 135 140   |     |
| CTT CTG GAC ACT AAG GGC AGA CTC TAT CGT TGG CGG TCG CCT GTC ATC | 480 |
| Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile |     |
| 145 150 155 160   |     |
| ATA GAG AAA AGG GGC AAA GTT GAG GTC GAA GGT CAC CTG ATC GAC CTC | 528 |
| Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu |     |
| 165 170 175   |     |
| AAA AGA GTT GTG CTT GAT GGT TCC GCG GCT ACC CCT GTA ACC AGA GTT | 576 |
| Lys Arg Val Val Leu Asp Gly Ser Ala Ala Thr Pro Val Thr Arg Val |     |
| 180 185 190   |     |
| TCA GCG GAA CAA TGG AGT CGT CCT TAG                             | 603 |
| Ser Ala Glu Gln Trp Ser Arg Pro                                 |     |
| 195 200   |     |



(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Cys | Leu | Thr | Ala | Gly | Cys | Cys | Ser | Gln | Leu | Leu | Phe | 1   | 5   | 10  | 15  |
| Leu | Trp | Cys | Ile | Val | Pro | Ser | Cys | Phe | Val | Ala | Leu | Val | Ser | Ala | Asn | 20  | 25  | 30  |     |
| Gly | Asn | Ser | Gly | Ser | Asn | Leu | Gln | Leu | Ile | Tyr | Asn | Leu | Thr | Leu | Cys | 35  | 40  | 45  |     |
| Glu | Leu | Asn | Gly | Thr | Asp | Trp | Leu | Ala | Asn | Lys | Phe | Asp | Trp | Ala | Val | 50  | 55  | 60  |     |
| Glu | Cys | Phe | Val | Ile | Phe | Pro | Val | Leu | Thr | His | Ile | Val | Ser | Tyr | Gly | 65  | 70  | 75  | 80  |
| Ala | Leu | Thr | Thr | Ser | His | Phe | Leu | Asp | Thr | Val | Gly | Leu | Val | Thr | Val | 85  | 90  | 95  |     |
| Ser | Thr | Ala | Gly | Phe | Val | His | Gly | Arg | Tyr | Val | Leu | Ser | Ser | Met | Tyr | 100 | 105 | 110 |     |
| Ala | Val | Cys | Ala | Leu | Ala | Ala | Leu | Ile | Cys | Phe | Val | Ile | Arg | Leu | Ala | 115 | 120 | 125 |     |
| Lys | Asn | Cys | Met | Ser | Trp | Arg | Tyr | Ser | Cys | Thr | Arg | Tyr | Thr | Asn | Phe | 130 | 135 | 140 |     |
| Leu | Leu | Asp | Thr | Lys | Gly | Arg | Leu | Tyr | Arg | Trp | Arg | Ser | Pro | Val | Ile | 145 | 150 | 155 | 160 |
| Ile | Glu | Lys | Arg | Gly | Lys | Val | Glu | Val | Glu | Gly | His | Leu | Ile | Asp | Leu | 165 | 170 | 175 |     |
| Lys | Arg | Val | Val | Leu | Asp | Gly | Ser | Ala | Ala | Thr | Pro | Val | Thr | Arg | Val | 180 | 185 | 190 |     |
| Ser | Ala | Glu | Gln | Trp | Ser | Arg | Pro | 195 | 200 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|   |     |
|---|-----|
| ATG GAG TCG TCC TTA GAT GAC TTC TGT CAT GAT AGC ACG GCT CCA CAA | 48  |
| Met Glu Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln |     |
| 1 5 10 15   |     |
| AAG GTG CTC TTG GCG TTT TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT | 96  |
| Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr |     |
| 20 25 30  |     |
| GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG | 144 |
| Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu |     |
| 35 40 45  |     |
| GTC TTC CTG AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG CAC | 192 |
| Val Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His |     |
| 50 55 60  |     |
| TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA | 240 |
| Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala |     |
| 65 70 75 80   |     |
| CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC | 288 |
| Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr |     |
| 85 90 95  |     |
| TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT | 336 |
| Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro |     |
| 100 105 110   |     |

|   |     |
|---|-----|
| GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT | 384 |
| Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn |     |
| 115 120 125   |     |
| GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC AAC | 432 |
| Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn |     |
| 130 135 140   |     |
| GGC ACA TTG GTG CCC GGG TTA AAA AGC CTC GTG TTG GGT GGC AGA AAA | 480 |
| Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys |     |
| 145 150 155 160   |     |
| GCT GTT AAA CAG GGA GTG GTA AAC CTT GTT AAA TAT GCC AAA         | 522 |
| Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys         |     |
| 165 170   |     |
| TAA   | 525 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Ser | Leu | Asp | Asp | Phe | Cys | His | Asp | Ser | Thr | Ala | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Val | Leu | Leu | Ala | Phe | Ser | Ile | Thr | Tyr | Thr | Pro | Val | Met | Ile | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Lys | Val | Ser | Arg | Gly | Arg | Leu | Leu | Gly | Leu | Leu | His | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Phe | Leu | Asn | Cys | Ala | Phe | Thr | Phe | Gly | Tyr | Met | Thr | Phe | Val | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Gln | Ser | Thr | Asn | Lys | Val | Ala | Leu | Thr | Met | Gly | Ala | Val | Val | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Leu | Trp | Gly | Val | Tyr | Ser | Ala | Ile | Glu | Thr | Trp | Lys | Phe | Ile | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Arg | Cys | Arg | Leu | Cys | Leu | Leu | Gly | Arg | Lys | Tyr | Ile | Leu | Ala | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn  
 115 120 125  
 Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn  
 130 135 140  
 Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys  
 145 150 155 160  
 Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|   |     |
|---|-----|
| ATG CCA AAT AAC ACC GGC AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC | 48  |
| Met Pro Asn Asn Thr Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly |     |
| 1 5 10 15   |     |
| CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAC | 96  |
| Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala His |     |
| 20 25 30  |     |
| CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA | 144 |
| Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys |     |
| 35 40 45  |     |
| AAC CCG GAG AAG CCC CAT TTC CCT CTA GCG ACT GAA GAT GAT GTC AGA | 192 |
| Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| CAT CAC TTT ACC CCT AGT GAG CGT CAA TTG TGT CTG TCG TCA ATC CAG | 240 |
| His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln |     |
| 65 70 75 80   |     |
| ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG | 288 |
| Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly |     |
| 85 90 95  |     |
| AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCT ACG CAT CAT ACT GTG | 336 |
| Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val |     |
| 100 105 110   |     |
| CGC CTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA                 | 372 |
| Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala                     |     |
| 115 120   |     |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|   |  |
|---|--|
| Met Pro Asn Asn Thr Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly |  |
| 1 5 10 15   |  |
| Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala His |  |
| 20 25 30  |  |
| Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys |  |
| 35 40 45  |  |
| Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg |  |
| 50 55 60  |  |
| His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln |  |
| 65 70 75 80   |  |
| Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly |  |
| 85 90 95  |  |
| Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val |  |
| 100 105 110   |  |
| Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala                     |  |
| 115 120   |  |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|   |     |
|---|-----|
| ATG AGA TGT TCT CAC AAA TTG GGG CGT TTC TTG ACT CCG CAC TCT TGC | 48  |
| Met Arg Cys Ser His Lys Leu Gly Arg Phe Leu Thr Pro His Ser Cys |     |
| 1 5 10 15   |     |
| TTC TGG TGG CTT TTT TTG CTG TGT ACC GGC TTG TCC TGG TCC TTT GCC | 96  |
| Phe Trp Trp Leu Phe Leu Leu Cys Thr Gly Leu Ser Trp Ser Phe Ala |     |
| 20 25 30  |     |
| GAT GGC AAC GGC GAC AGC TCG ACA TAC CAA TAC ATA TAT AAC TTG ACG | 144 |
| Asp Gly Asn Gly Asp Ser Ser Thr Tyr Gln Tyr Ile Tyr Asn Leu Thr |     |
| 35 40 45  |     |
| ATA TGC GAG CTG AAT GGG ACC GAC TGG TTG TCC AGC CAT TTT GGT TGG | 192 |
| Ile Cys Glu Leu Asn Gly Thr Asp Trp Leu Ser Ser His Phe Gly Trp |     |
| 50 55 60  |     |
| GCA GTC GAG ACC TTT GTG CTT TAC CCG GTT GCC ACT CAT ATC CTC TCA | 240 |
| Ala Val Glu Thr Phe Val Leu Tyr Pro Val Ala Thr His Ile Leu Ser |     |
| 65 70 75 80   |     |
| CTG GGT TTT CTC ACA ACA AGC CAT TTT TTT GAC GCG CTC GGT CTC GGC | 288 |
| Leu Gly Phe Leu Thr Thr Ser His Phe Phe Asp Ala Leu Gly Leu Gly |     |
| 85 90 95  |     |
| GCT GTA TCC ACT GCA GGA TTT GTT GGC GGG CGG TAC GTA CTC TGC AGC | 336 |
| Ala Val Ser Thr Ala Gly Phe Val Gly Gly Arg Tyr Val Leu Cys Ser |     |
| 100 105 110   |     |

|   |     |
|---|-----|
| GTC TAC GGC GCT TGT GCT TTC GCA GCG TTC GTA TGT TTT GTC ATC CGT | 384 |
| Val Tyr Gly Ala Cys Ala Phe Ala Ala Phe Val Cys Phe Val Ile Arg |     |
| 115 120 125   |     |
| GCT GCT AAA AAT TGC ATG GCC TGC CGC TAT GCC CGT ACC CGG TTT ACC | 432 |
| Ala Ala Lys Asn Cys Met Ala Cys Arg Tyr Ala Arg Thr Arg Phe Thr |     |
| 130 135 140   |     |
| AAC TTC ATT GTG GAC GAC CGG GGG AGA GTT CAT CGA TGG AAG TCT CCA | 480 |
| Asn Phe Ile Val Asp Asp Arg Gly Arg Val His Arg Trp Lys Ser Pro |     |
| 145 150 155 160   |     |
| ATA GTG GTA GAA AAA TTG GGC AAA GCC GAA GTC GAT GGC AAC CTC GTC | 528 |
| Ile Val Val Glu Lys Leu Gly Lys Ala Glu Val Asp Gly Asn Leu Val |     |
| 165 170 175   |     |
| ACC ATC AAA CAT GTC GTC CTC GAA GGG GTT AAA GCT CAA CCC TTG ACG | 576 |
| Thr Ile Lys His Val Val Leu Glu Gly Val Lys Ala Gln Pro Leu Thr |     |
| 180 185 190   |     |
| AGG ACT TCG GCT GAG CAA TGG GAG GCC TAG                         | 606 |
| Arg Thr Ser Ala Glu Gln Trp Glu Ala                             |     |
| 195 200   |     |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

|   |
|---|
| Met Arg Cys Ser His Lys Leu Gly Arg Phe Leu Thr Pro His Ser Cys |
| 1 5 10 15   |
| Phe Trp Trp Leu Phe Leu Leu Cys Thr Gly Leu Ser Trp Ser Phe Ala |
| 20 25 30  |
| Asp Gly Asn Gly Asp Ser Ser Thr Tyr Gln Tyr Ile Tyr Asn Leu Thr |
| 35 40 45  |
| Ile Cys Glu Leu Asn Gly Thr Asp Trp Leu Ser Ser His Phe Gly Trp |
| 50 55 60  |
| Ala Val Glu Thr Phe Val Leu Tyr Pro Val Ala Thr His Ile Leu Ser |
| 65 70 75 80   |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Gly | Phe | Leu | Thr | Thr | Ser | His | Phe | Phe | Asp | Ala | Leu | Gly | Leu | Gly |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Val | Ser | Thr | Ala | Gly | Phe | Val | Gly | Gly | Arg | Tyr | Val | Leu | Cys | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Tyr | Gly | Ala | Cys | Ala | Phe | Ala | Ala | Phe | Val | Cys | Phe | Val | Ile | Arg |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Ala | Lys | Asn | Cys | Met | Ala | Cys | Arg | Tyr | Ala | Arg | Thr | Arg | Phe | Thr |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asn | Phe | Ile | Val | Asp | Asp | Arg | Gly | Arg | Val | His | Arg | Trp | Lys | Ser | Pro |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ile | Val | Val | Glu | Lys | Leu | Gly | Lys | Ala | Glu | Val | Asp | Gly | Asn | Leu | Val |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Thr | Ile | Lys | His | Val | Val | Leu | Glu | Gly | Val | Lys | Ala | Gln | Pro | Leu | Thr |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Arg | Thr | Ser | Ala | Glu | Gln | Trp | Glu | Ala |     |     |     |     |     |     |     |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|   |     |
|---|-----|
| TGGGCTGGCA TTCTTGAGGC ATCCCAGTGT TTGAATTGGA AGAATGCGTG GTGAATGGCA | 60  |
| CTGATTGACA TTGTGCCTCT AAGTCACCTA TTCAATTAGG GCGACCGTGT GGGGGTAAGA | 120 |
| TTTAATTGGC GAGAACCACA CGGCCGAAAT TAAAAAAAAA AAAA                  | 164 |



(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|   |     |
|---|-----|
| ATG GGA GGC CTA GAC GAT TTT TGC AAC GAT CCT ATC GCC GCA CAA AAG | 48  |
| Met Gly Gly Leu Asp Asp Phe Cys Asn Asp Pro Ile Ala Ala Gln Lys |     |
| 1 5 10 15   |     |
| CTC GTG CTA GCC TTT AGC ATC ACA TAC ACA CCT ATA ATG ATA TAC GCC | 96  |
| Leu Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Ile Met Ile Tyr Ala |     |
| 20 25 30  |     |
| CTT AAG GTG TCA CGC GGC CGA CTC CTG GGG CTG TTG CAC ATC CTA ATA | 144 |
| Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile |     |
| 35 40 45  |     |
| TTT CTG AAC TGT TCC TTT ACA TTC GGA TAC ATG ACA TAT GTG CAT TTT | 192 |
| Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe |     |
| 50 55 60  |     |
| CAA TCC ACC AAC CGT GTC GCA CTT ACC CTG GGG GCT GTT GTC GCC CTT | 240 |
| Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu |     |
| 65 70 75 80   |     |
| CTG TGG GGT GTT TAC AGC TTC ACA GAG TCA TGG AAG TTT ATC ACT TCC | 288 |
| Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser |     |
| 85 90 95  |     |
| AGA TGC AGA TTG TGT TGC CTT GGC CGG CGA TAC ATT CTG GCC CCT GCC | 336 |
| Arg Cys Arg Leu Cys Cys Leu Gly Arg Arg Tyr Ile Leu Ala Pro Ala |     |
| 100 105 110   |     |

|   |     |
|---|-----|
| CAT CAC GTA GAA AGT GCT GCA GGT CTC CAT TCA ATC TCA GCG TCT GGT | 384 |
| His His Val Glu Ser Ala Ala Gly Leu His Ser Ile Ser Ala Ser Gly |     |
| 115 120 125   |     |
| AAC CGA GCA TAC GCT GTG AGA AAG CCC GGA CTA ACA TCA GTG AAC GGC | 432 |
| Asn Arg Ala Tyr Ala Val Arg Lys Pro Gly Leu Thr Ser Val Asn Gly |     |
| 130 135 140   |     |
| ACT CTA GTA CCA GGA CTT CGG AGC CTC GTG CTG GGC GGC AAA CGA GCT | 480 |
| Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Arg Ala |     |
| 145 150 155 160   |     |
| GTT AAA CGA GGA GTG GTT AAC CTC GTC AAG TAT GGC CGG TAA         | 522 |
| Val Lys Arg Gly Val Val Asn Leu Val Lys Tyr Gly Arg             |     |
| 165 170   |     |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|   |  |
|---|--|
| Met Gly Gly Leu Asp Asp Phe Cys Asn Asp Pro Ile Ala Ala Gln Lys |  |
| 1 5 10 15   |  |
| Leu Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Ile Met Ile Tyr Ala |  |
| 20 25 30  |  |
| Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile |  |
| 35 40 45  |  |
| Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe |  |
| 50 55 60  |  |
| Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu |  |
| 65 70 75 80   |  |
| Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser |  |
| 85 90 95  |  |
| Arg Cys Arg Leu Cys Cys Leu Gly Arg Arg Tyr Ile Leu Ala Pro Ala |  |
| 100 105 110   |  |
| His His Val Glu Ser Ala Ala Gly Leu His Ser Ile Ser Ala Ser Gly |  |
| 115 120 125   |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Arg | Ala | Tyr | Ala | Val | Arg | Lys | Pro | Gly | Leu | Thr | Ser | Val | Asn | Gly |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Leu | Val | Pro | Gly | Leu | Arg | Ser | Leu | Val | Leu | Gly | Gly | Lys | Arg | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Lys | Arg | Gly | Val | Val | Asn | Leu | Val | Lys | Tyr | Gly | Arg |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GCC | GGT | AAA | AAC | CAG | AGC | CAG | AAG | AAA | AAG | AAA | AGT | ACA | GCT | CCG | 48  |
| Met | Ala | Gly | Lys | Asn | Gln | Ser | Gln | Lys | Lys | Lys | Lys | Ser | Thr | Ala | Pro |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| ATG | GGG | AAT | GGC | CAG | CCA | GTC | AAT | CAA | CTG | TGC | CAG | TTG | CTG | GGT | GCA | 96  |
| Met | Gly | Asn | Gly | Gln | Pro | Val | Asn | Gln | Leu | Cys | Gln | Leu | Leu | Gly | Ala |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| ATG | ATA | AAG | TCC | CAG | CGC | CAG | CAA | CCT | AGG | GGA | GGA | CAG | GCC | AAA | AAG | 144 |
| Met | Ile | Lys | Ser | Gln | Arg | Gln | Gln | Pro | Arg | Gly | Gly | Gln | Ala | Lys | Lys |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| AAA | AAG | CCT | GAG | AAG | CCA | CAT | TTT | CCC | CTG | GCT | GCT | GAA | GAT | GAC | ATC | 192 |
| Lys | Lys | Pro | Glu | Lys | Pro | His | Phe | Pro | Leu | Ala | Ala | Glu | Asp | Asp | Ile |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CGG | CAC | CAC | CTC | ACC | CAG | ACT | GAA | CGC | TCC | CTC | TGC | TTG | CAA | TCG | ATC | 240 |
| Arg | His | His | Leu | Thr | Gln | Thr | Glu | Arg | Ser | Leu | Cys | Leu | Gln | Ser | Ile |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

|   |     |
|---|-----|
| CAG ACG GCT TTC AAT CAA GGC GCA GGA ACT GCG TCG CTT TCA TCC AGC | 288 |
| Gln Thr Ala Phe Asn Gln Gly Ala Gly Thr Ala Ser Leu Ser Ser Ser |     |
| 85 90 95  |     |
| GGG AAG GTC AGT TTT CAG GTT GAG TTT ATG CTG CCG GTT GCT CAT ACA | 336 |
| Gly Lys Val Ser Phe Gln Val Glu Phe Met Leu Pro Val Ala His Thr |     |
| 100 105 110   |     |
| GTG CGC CTG ATT CGC GTG ACT TCT ACA TCC GCC AGT CAG GGT GCA AGT | 384 |
| Val Arg Leu Ile Arg Val Thr Ser Thr Ser Ala Ser Gln Gly Ala Ser |     |
| 115 120 125   |     |
| TAA   | 387 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

|   |  |
|---|--|
| Met Ala Gly Lys Asn Gln Ser Gln Lys Lys Lys Lys Ser Thr Ala Pro |  |
| 1 5 10 15   |  |
| Met Gly Asn Gly Gln Pro Val Asn Gln Leu Cys Gln Leu Leu Gly Ala |  |
| 20 25 30  |  |
| Met Ile Lys Ser Gln Arg Gln Gln Pro Arg Gly Gly Gln Ala Lys Lys |  |
| 35 40 45  |  |
| Lys Lys Pro Glu Lys Pro His Phe Pro Leu Ala Ala Glu Asp Asp Ile |  |
| 50 55 60  |  |
| Arg His His Leu Thr Gln Thr Glu Arg Ser Leu Cys Leu Gln Ser Ile |  |
| 65 70 75 80   |  |
| Gln Thr Ala Phe Asn Gln Gly Ala Gly Thr Ala Ser Leu Ser Ser Ser |  |
| 85 90 95  |  |
| Gly Lys Val Ser Phe Gln Val Glu Phe Met Leu Pro Val Ala His Thr |  |
| 100 105 110   |  |
| Val Arg Leu Ile Arg Val Thr Ser Thr Ser Ala Ser Gln Gly Ala Ser |  |
| 115 120 125   |  |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

|   |     |
|---|-----|
| TTTGACAGTC AGGTGAATGG CCGCGATTGG CGTGTGGCCT CTGAGTCACC TATTCAATTA | 60  |
| GGGCGATCAC ATGGGGGTCA TACTTAATCA GGCAGGAACC ATGTGACCGA AATTAAAAAA | 120 |
| AAAAAAA   | 127 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

|                              |    |
|------------------------------|----|
| GGGGATCCGG TATTTGGCAA TGTGTC | 26 |
|------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGTGTTTTCC ACGAGAACCG CTTAAGGG

28

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGGATCCAG AGTTTCAGCG G

21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGTTAGTCG ACACGGTCTT AAGGG

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGGATCCTT GTTAAATATG CC

22

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTTACGCACC ACTTAAGGG

19

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AATGGGGCTT CTCCGG

16

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 886 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|  |     |
|--|-----|
| ATGGAGTCGT CCTTAGATGA CTTCTGTCAT GATAGCACGG CTCCACAAAA GGTGCTCTTG  | 60  |
| GCGTTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA  | 120 |
| CTGCTAGGGC TTCTGCACCT TTTGGTCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG  | 180 |
| ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA  | 240 |
| CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT  | 300 |
| TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA  | 360 |
| GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC  | 420 |
| ACTACGGTCA ACGGCACATT GGTGCCCCGGG TTAAAAAGCC TCGTGTTGGG TGGCAGAAAA | 480 |
| GCTGTTAAAC AGGGAGTGGT AAACCTTGTT AAATATGCCA AATAACACCG GCAAGCAGCA  | 540 |
| GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT  | 600 |
| CATCGCTCAC CAAAACCACT CCAGAGGCAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA  | 660 |
| CCCGGAGAAG CCCCATTTCC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC  | 720 |
| TAGTGAGCGT CAATTGTGTC TGTCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC  | 780 |
| TTGCACCCTG TCAGATTCAG GGAGGATAAG TTACTGTG GAGTTTAGTT TGCCTACGCA    | 840 |
| TCATACTGTG CGCCTGATCC GCGTCACAGC ATCACCTCA GCATGA                  | 886 |

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-1894



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|  |     |
|--|-----|
| ATGGGGTCGT CCTTAGATGA CTTCTGCCAT GATAGTACGG CTCCACAAAA GGTGCTTTTG  | 60  |
| GCGTTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA  | 120 |
| CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG  | 180 |
| ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA  | 240 |
| CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT  | 300 |
| TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA  | 360 |
| GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC  | 420 |
| ACTACGGTCA ACGGCACATT GGTGCCCCGGG TTGAAAAGCC TCGTGTTGGG TGGCAGAAAA | 480 |
| GCTGTTAAAC AGGGAGTGGT AAACCTTGTC AAATATGCCA AATAACAACG GCAAGCAGCA  | 540 |
| GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT  | 600 |
| CATCGCTCAG CAAAACCAGT CCAGAGGCAA GGGACCGGGA AAGAAAAACA AGAAGAAAAA  | 660 |
| CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCCC  | 720 |
| TAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC  | 780 |
| TTGCACCCTG TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCAACGCA  | 840 |
| TCATACTGTG CGCTTGATCC GCGTCACAGC ATCACCTCA GCATGA                  | 886 |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|  |     |
|--|-----|
| ATGGGGTCGT CCTTAGATGA CTTCTGTCAT GACAGCACGG CTCCACAAAA GGTGCTTTTG  | 60  |
| GCGTTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TGAAGGTGAG TCGCGGCCGA  | 120 |
| CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG  | 180 |
| ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCACTCA CTATGGGAGC AGTAGTTGCA  | 240 |
| CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT  | 300 |
| TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA  | 360 |
| GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTTCGGCG TCCCGGCTCC  | 420 |
| ACTACGGTCA ACGGCACATT GGTGCCCCGGG TTGAAAAGCC TCGTGTTGGG TGGCAGAAAA | 480 |
| GCTGTTAAAC AGGGAGTGGT AAACCTTGTC AAATATGCCA AATAACAACG GTAAGCAGCA  | 540 |
| GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGCAAGAT  | 600 |
| CATCGCTCAG CAAAATCAGT CCAGAGGCAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA  | 660 |
| CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC  | 720 |
| TAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC  | 780 |
| TTGCACCCTG TCAGATTCAG GGAGGATAAG TTACTGTG GAGTTTAGTT TGCCTACGCA    | 840 |
| TCATACTGTG CGCCTGATCC GCGTCACAGC ATCACCCTCA GCATGA                 | 886 |

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

|  |     |
|--|-----|
| ATGGGGTCGT CCTTAGATGA CTTCTGTTAT GATAGTACGG CTCCACAAAA GGTGCTTTTG  | 60  |
| GCATTTTCTA TTACCTACAC GCCAGTAATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA  | 120 |
| CTGCTAGGGC TTCTGCACCT TTTGATTTTC CTGAACTGTG CTTTCACCTT CGGGTACATG  | 180 |
| ACATTCATGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA  | 240 |
| CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT  | 300 |
| TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA  | 360 |
| GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC  | 420 |
| ACTACGGTCA ACGGCACATT GGTGCCCCGGG TTGAAAAGCC TCGTGTTGGG TGGCAGAAAA | 480 |
| GCTGTTAAAC AGGGAGTGGT AAACCTTGTC AAATATGCCA AATAACAACG GCAAGCAGCA  | 540 |
| GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT  | 600 |
| CATCGCCCAG CAAAACCAGT CTAGAGGCAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA  | 660 |
| CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC  | 720 |
| TAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAAAGTGCC TTTAATCAAG GCGCTGGGAC  | 780 |
| TTGCACCCTG TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCTACGCA  | 840 |
| TCATACTGTG CGCTTGATCC GCGTCACAGC ATCACCTCA GCATGA                  | 886 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

|  |     |
|--|-----|
| ATGGGGTCGT CCTTAGATGA CTTCTGCCAT GATAGCACGG CTCCACAAAA GGTGCTTTTG  | 60  |
| GCGTTCTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAAGTAAG TCGCGGCCGA  | 120 |
| CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTAAATTGTG CTTTCACCTT CGGGTACATG  | 180 |
| ACATTCGTGC ACTTTCAGAG CACAAACAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA  | 240 |
| CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT  | 300 |
| TTGTGCTTGC TAGGCCGCAA GTACATTTTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA  | 360 |
| GGCTTTCATC CGATAGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC  | 420 |
| ACTACGGTTA ACGGCACATT GGTGCCCCGGG TTGAAAAGCC TCGTGTTGGG TGGCAGAAAA | 480 |
| GCTGTCAAAC AGGGAGTGGT AAACCTTGTT AAATATGCCA AATAACAACG GCAAGCAGCA  | 540 |
| GAAGAAAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT  | 600 |
| CATCGCTCAG CAAAACCAGT CCAGAGGCAA GGGACCGGGA AAGAAAAACA AGAAGAAAAA  | 660 |
| CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCTC  | 720 |
| TGGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACAGCC TTTAATCAAG GCGCTGGAAC  | 780 |
| TTGTACCCTG TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCGACGCA  | 840 |
| TCATACTGTG CGCTTGATCC GCGTCACAGC GTCACCCTCA GCATGA                 | 886 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

|  |     |
|--|-----|
| ATGGGGTCGT CCCTAGACGA CTTTGTGCAAT GATAGCACGG CTCCACAAAA GGTGCTTTTG   | 60  |
| GCGTTTTCTA TTACCTACAC GCCGGTGATG ATATATGCTC TAAAGGTAAG TCGCGGCCGA    | 120 |
| CTGCTAGGGC TTCTGCACCT TTTGATTTTT CTGAATTGTG CTTTTACTTT CGGGTACATG    | 180 |
| ACATTCGTGC ACTTTGAGAG CACAAATAGG GTCGCGCTCA CTATGGGAGC AGTAGTCGCA    | 240 |
| CTTCTCTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT    | 300 |
| TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA GAGTGCCGCA    | 360 |
| GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC    | 420 |
| ACTACGGTTA ACGGCACATT GGTGCCCCGGG TTGAGAAGCC TCGTGTGTTGGG TGGCAAAAAA | 480 |
| GCTGTTAAGC AGGGAGTGGT AAACCTTGTT AAATATGCCA AATAACAACG GCAAGCAGCA    | 540 |
| GAAGAAAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTC TGCCAAATGC TGGGTAAGAT    | 600 |
| CATCGCCCAG CAAAACCACT CCAGAGGTAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA    | 660 |
| CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCCC    | 720 |
| CAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACTGCC TTTAATCAGG GCGCTGGGAC    | 780 |
| CTGTATCCTA TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCGACGCA    | 840 |
| TCATACTGTG CGCCTGATTC GCGTCACGGC ACCACCCTCA GCATGA                   | 886 |

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

|   |    |
|---|----|
| ATGGGAGGCC TAGACGATTT TTGCAACGAT CCTATCGCCG CACAAAAGCT CGTGCTAGCC | 60 |
|---|----|

|   |     |
|---|-----|
| TTTAGCATCA CATAACACC TATAATGATA TACGCCCTTA AGGTGTCACG CGGCCGACTC  | 120 |
| CTGGGGCTGT TGCACATCCT AATATTTCTG AACTGTTCTT TTACATTCGG ATACATGACA | 180 |
| TATGTGCATT TTCAATCCAC CAACCGTGTC GCACTTACCC TGGGGGCTGT TGTCGCCCTT | 240 |
| CTGTGGGGTG TTTACAGCTT CACAGAGTCA TGGAAGTTTA TCACTTCCAG ATGCAGATTG | 300 |
| TGTTGCCTTG GCCGGCGATA CATTCTGGCC CCTGCCCATC ACGTAGAAAG TGCTGCAGGT | 360 |
| CTCCATTCAA TCTCAGCGTC TGGTAACCGA GCATACGCTG TGAGAAAGCC CGGACTAACA | 420 |
| TCAGTGAACG GCACTCTAGT ACCAGGACTT CGGAGCCTCG TGCTGGGCGG CAAACGAGCT | 480 |
| GTTAAACGAG GAGTGGTTAA CCTCGTCAAG TATGGCCGGT AAAAACCAGA GCCAGAAGAA | 540 |
| AAAGAAAAGT ACAGCTCCGA TGGGGAATGG CCAGCCAGTC AATCAACTGT GCCAGTTGCT | 600 |
| GGGTGCAATG ATAAAGTCCC AGCGCCAGCA ACCTAGGGGA GGACAGGCCA AAAAGAAAAA | 660 |
| GCCTGAGAAG CCACATTTTC CCCTGGCTGC TGAAGATGAC ATCCGGCACC ACCTCACCCA | 720 |
| GACTGAACGC TCCCTCTGCT TGCAATCGAT CCAGACGGCT TTCAATCAAG GCGCAGGAAC | 780 |
| TGCGTCGCTT TCATCCAGCG GGAAGGTCAG TTTTCAGGTT GAGTTTATGC TGCCGGTTGC | 840 |
| TCATACAGTG CGCCTGATTC GCGTGACTTC TACATCCGCC AGTCAGGGTG CAAGTTAA   | 898 |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-1894

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

[illegible]

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ser | Ser | Leu | Asp | Asp | Phe | Cys | His | Asp | Ser | Thr | Ala | Pro | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Val | Leu | Leu | Ala | Phe | Ser | Ile | Thr | Tyr | Thr | Pro | Val | Met | Ile | Tyr |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Leu | Lys | Val | Ser | Arg | Gly | Arg | Leu | Leu | Gly | Leu | Leu | His | Leu | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Phe | Leu | Asn | Cys | Ala | Phe | Thr | Phe | Gly | Tyr | Met | Thr | Phe | Val | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Gln | Ser | Thr | Asn | Lys | Val | Ala | Leu | Thr | Met | Gly | Ala | Val | Val | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Leu | Trp | Gly | Val | Tyr | Ser | Ala | Ile | Glu | Thr | Trp | Lys | Phe | Ile | Thr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Arg | Cys | Arg | Leu | Cys | Leu | Leu | Gly | Arg | Lys | Tyr | Ile | Leu | Ala | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | His | His | Val | Glu | Ser | Ala | Ala | Gly | Phe | His | Pro | Ile | Ala | Ala | Asn |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asp | Asn | His | Ala | Phe | Val | Val | Arg | Arg | Pro | Gly | Ser | Thr | Thr | Val | Asn |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Thr | Leu | Val | Pro | Gly | Leu | Lys | Ser | Leu | Val | Leu | Gly | Gly | Arg | Lys |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Val | Lys | Gln | Gly | Val | Val | Asn | Leu | Val | Lys | Tyr | Ala | Lys |     |     |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

|   |     |
|---|-----|
| ATG GGG TCG TCC TTA GAT GAC TTC TGT CAT GAC AGC ACG GCT CCA CAA | 48  |
| Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln |     |
| 1 5 10 15   |     |
| AAG GTG CTT TTG GCG TTT TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT | 96  |
| Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr |     |
| 20 25 30  |     |
| GCC CTG AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG | 144 |
| Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu |     |
| 35 40 45  |     |
| ATC TTC CTG AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG CAC | 192 |
| Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His |     |
| 50 55 60  |     |
| TTT CAG AGT ACA AAT AAG GTC GCA CTC ACT ATG GGA GCA GTA GTT GCA | 240 |
| Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala |     |
| 65 70 75 80   |     |
| CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC | 288 |
| Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr |     |
| 85 90 95  |     |
| TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT | 336 |
| Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro |     |
| 100 105 110   |     |
| GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT | 384 |
| Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn |     |
| 115 120 125   |     |
| GAT AAC CAC GCA TTT GTC GTT CGG CGT CCC GGC TCC ACT ACG GTC AAC | 432 |
| Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn |     |
| 130 135 140   |     |

GGC ACA TTG GTG CCC GGG TTG AAA AGC CTC GTG TTG GGT GGC AGA AAA 480  
Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys  
145 150 155 160

GCT GTT AAA CAG GGA GTG GTA AAC CTT GTC AAA TAT GCC AAA 522  
Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys  
165 170

TAA 525

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln  
1 5 10 15  
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr  
20 25 30  
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu  
35 40 45  
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His  
50 55 60  
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala  
65 70 75 80  
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr  
85 90 95  
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro  
100 105 110  
Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn  
115 120 125  
Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn  
130 135 140  
Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys  
145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys  
165 170

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|   |     |
|---|-----|
| ATG GGG TCG TCC TTA GAT GAC TTC TGT TAT GAT AGT ACG GCT CCA CAA | 48  |
| Met Gly Ser Ser Leu Asp Asp Phe Cys Tyr Asp Ser Thr Ala Pro Gln |     |
| 1 5 10 15   |     |
| AAG GTG CTT TTG GCA TTT TCT ATT ACC TAC ACG CCA GTA ATG ATA TAT | 96  |
| Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr |     |
| 20 25 30  |     |
| GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG | 144 |
| Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu |     |
| 35 40 45  |     |
| ATT TTC CTG AAC TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC ATG CAC | 192 |
| Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Met His |     |
| 50 55 60  |     |
| TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA | 240 |
| Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala |     |
| 65 70 75 80   |     |
| CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC | 288 |
| Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr |     |
| 85 90 95  |     |

|   |     |
|---|-----|
| TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT | 336 |
| Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro |     |
| 100 105 110   |     |
| GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT | 384 |
| Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn |     |
| 115 120 125   |     |
| GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC AAC | 432 |
| Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn |     |
| 130 135 140   |     |
| GGC ACA TTG GTG CCC GGG TTG AAA AGC CTC GTG TTG GGT GGC AGA AAA | 480 |
| Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys |     |
| 145 150 155 160   |     |
| GCT GTT AAA CAG GGA GTG GTA AAC CTT GTC AAA TAT GCC AAA         | 522 |
| Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys         |     |
| 165 170   |     |
| TAA   | 525 |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|   |  |
|---|--|
| Met Gly Ser Ser Leu Asp Asp Phe Cys Tyr Asp Ser Thr Ala Pro Gln |  |
| 1 5 10 15   |  |
| Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr |  |
| 20 25 30  |  |
| Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu |  |
| 35 40 45  |  |
| Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Met His |  |
| 50 55 60  |  |
| Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala |  |
| 65 70 75 80   |  |
| Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr |  |
| 85 90 95  |  |

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro  
100 105 110

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn  
115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn  
130 135 140

Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys  
145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys  
165 170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|   |     |
|---|-----|
| ATG GGG TCG TCC TTA GAT GAC TTC TGC CAT GAT AGC ACG GCT CCA CAA | 48  |
| Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln |     |
| 1 5 10 15   |     |
| AAG GTG CTT TTG GCG TTC TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT | 96  |
| Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr |     |
| 20 25 30  |     |
| GCC CTA AAA GTA AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG | 144 |
| Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu |     |
| 35 40 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATC | TTC | CTA | AAT | TGT | GCT | TTC | ACC | TTC | GGG | TAC | ATG | ACA | TTC | GTG | CAC | 192 |
| Ile | Phe | Leu | Asn | Cys | Ala | Phe | Thr | Phe | Gly | Tyr | Met | Thr | Phe | Val | His |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| TTT | CAG | AGC | ACA | AAC | AAG | GTC | GCG | CTC | ACT | ATG | GGA | GCA | GTA | GTT | GCA | 240 |
| Phe | Gln | Ser | Thr | Asn | Lys | Val | Ala | Leu | Thr | Met | Gly | Ala | Val | Val | Ala |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| CTC | CTT | TGG | GGG | GTG | TAC | TCA | GCC | ATA | GAA | ACC | TGG | AAA | TTC | ATC | ACC | 288 |
| Leu | Leu | Trp | Gly | Val | Tyr | Ser | Ala | Ile | Glu | Thr | Trp | Lys | Phe | Ile | Thr |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| TCC | AGA | TGC | CGT | TTG | TGC | TTG | CTA | GGC | CGC | AAG | TAC | ATT | TTG | GCC | CCT | 336 |
| Ser | Arg | Cys | Arg | Leu | Cys | Leu | Leu | Gly | Arg | Lys | Tyr | Ile | Leu | Ala | Pro |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GCC | CAC | CAC | GTT | GAA | AGT | GCC | GCA | GGC | TTT | CAT | CCG | ATA | GCG | GCA | AAT | 384 |
| Ala | His | His | Val | Glu | Ser | Ala | Ala | Gly | Phe | His | Pro | Ile | Ala | Ala | Asn |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| GAT | AAC | CAC | GCA | TTT | GTC | GTC | CGG | CGT | CCC | GGC | TCC | ACT | ACG | GTT | AAC | 432 |
| Asp | Asn | His | Ala | Phe | Val | Val | Arg | Arg | Pro | Gly | Ser | Thr | Thr | Val | Asn |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| GGC | ACA | TTG | GTG | CCC | GGG | TTG | AAA | AGC | CTC | GTG | TTG | GGT | GGC | AGA | AAA | 480 |
| Gly | Thr | Leu | Val | Pro | Gly | Leu | Lys | Ser | Leu | Val | Leu | Gly | Gly | Arg | Lys |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| GCT | GTC | AAA | CAG | GGA | GTG | GTA | AAC | CTT | GTT | AAA | TAT | GCC | AAA |     |     | 522 |
| Ala | Val | Lys | Gln | Gly | Val | Val | Asn | Leu | Val | Lys | Tyr | Ala | Lys |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |
| TAA |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 525 |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ser | Ser | Leu | Asp | Asp | Phe | Cys | His | Asp | Ser | Thr | Ala | Pro | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Val | Leu | Leu | Ala | Phe | Ser | Ile | Thr | Tyr | Thr | Pro | Val | Met | Ile | Tyr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Lys | Val | Ser | Arg | Gly | Arg | Leu | Leu | Gly | Leu | Leu | His | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Phe | Leu | Asn | Cys | Ala | Phe | Thr | Phe | Gly | Tyr | Met | Thr | Phe | Val | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Gln | Ser | Thr | Asn | Lys | Val | Ala | Leu | Thr | Met | Gly | Ala | Val | Val | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Leu | Trp | Gly | Val | Tyr | Ser | Ala | Ile | Glu | Thr | Trp | Lys | Phe | Ile | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Arg | Cys | Arg | Leu | Cys | Leu | Leu | Gly | Arg | Lys | Tyr | Ile | Leu | Ala | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | His | His | Val | Glu | Ser | Ala | Ala | Gly | Phe | His | Pro | Ile | Ala | Ala | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Asn | His | Ala | Phe | Val | Val | Arg | Arg | Pro | Gly | Ser | Thr | Thr | Val | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Thr | Leu | Val | Pro | Gly | Leu | Lys | Ser | Leu | Val | Leu | Gly | Gly | Arg | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Val | Lys | Gln | Gly | Val | Val | Asn | Leu | Val | Lys | Tyr | Ala | Lys |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|   |     |
|---|-----|
| ATG GGG TCG TCC CTA GAC GAC TTT TGC AAT GAT AGC ACG GCT CCA CAA | 48  |
| Met Gly Ser Ser Leu Asp Asp Phe Cys Asn Asp Ser Thr Ala Pro Gln |     |
| 1 5 10 15   |     |
| AAG GTG CTT TTG GCG TTT TCT ATT ACC TAC ACG CCG GTG ATG ATA TAT | 96  |
| Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr |     |
| 20 25 30  |     |
| GCT CTA AAG GTA AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG | 144 |
| Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu |     |
| 35 40 45  |     |
| ATT TTT CTG AAT TGT GCT TTT ACT TTC GGG TAC ATG ACA TTC GTG CAC | 192 |
| Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His |     |
| 50 55 60  |     |
| TTT GAG AGC ACA AAT AGG GTC GCG CTC ACT ATG GGA GCA GTA GTC GCA | 240 |
| Phe Glu Ser Thr Asn Arg Val Ala Leu Thr Met Gly Ala Val Val Ala |     |
| 65 70 75 80   |     |
| CTT CTC TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC | 288 |
| Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr |     |
| 85 90 95  |     |
| TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT | 336 |
| Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro |     |
| 100 105 110   |     |
| GCC CAC CAC GTT GAG AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT | 384 |
| Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn |     |
| 115 120 125   |     |
| GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTT AAC | 432 |
| Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn |     |
| 130 135 140   |     |
| GGC ACA TTG GTG CCC GGG TTG AGA AGC CTC GTG TTG GGT GGC AAA AAA | 480 |
| Gly Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Lys |     |
| 145 150 155 160   |     |
| GCT GTT AAG CAG GGA GTG GTA AAC CTT GTT AAA TAT GCC AAA         | 522 |
| Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys         |     |
| 165 170   |     |
| TAA   | 525 |



(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ser | Ser | Leu | Asp | Asp | Phe | Cys | Asn | Asp | Ser | Thr | Ala | Pro | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Val | Leu | Leu | Ala | Phe | Ser | Ile | Thr | Tyr | Thr | Pro | Val | Met | Ile | Tyr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Leu | Lys | Val | Ser | Arg | Gly | Arg | Leu | Leu | Gly | Leu | Leu | His | Leu | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Phe | Leu | Asn | Cys | Ala | Phe | Thr | Phe | Gly | Tyr | Met | Thr | Phe | Val | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Glu | Ser | Thr | Asn | Arg | Val | Ala | Leu | Thr | Met | Gly | Ala | Val | Val | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Leu | Trp | Gly | Val | Tyr | Ser | Ala | Ile | Glu | Thr | Trp | Lys | Phe | Ile | Thr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Arg | Cys | Arg | Leu | Cys | Leu | Leu | Gly | Arg | Lys | Tyr | Ile | Leu | Ala | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | His | His | Val | Glu | Ser | Ala | Ala | Gly | Phe | His | Pro | Ile | Ala | Ala | Asn |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asp | Asn | His | Ala | Phe | Val | Val | Arg | Arg | Pro | Gly | Ser | Thr | Thr | Val | Asn |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Thr | Leu | Val | Pro | Gly | Leu | Arg | Ser | Leu | Val | Leu | Gly | Gly | Lys | Lys |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Val | Lys | Gln | Gly | Val | Val | Asn | Leu | Val | Lys | Tyr | Ala | Lys |     |     |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 372 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-1894

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

|   |     |
|---|-----|
| ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC | 48  |
| Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly |     |
| 1 5 10 15   |     |
| CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAG | 96  |
| Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln |     |
| 20 25 30  |     |
| CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAC AAG AAG AAA | 144 |
| Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys |     |
| 35 40 45  |     |
| AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA | 192 |
| Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg |     |
| 50 55 60  |     |
| CAT CAC TTC ACC CCT AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG | 240 |
| His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln |     |
| 65 70 75 80   |     |
| ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG | 288 |
| Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly |     |
| 85 90 95  |     |
| AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCA ACG CAT CAT ACT GTG | 336 |
| Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val |     |
| 100 105 110   |     |
| CGC TTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA                 | 372 |
| Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala                     |     |
| 115 120   |     |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Asn | Asn | Asn | Gly | Lys | Gln | Gln | Lys | Arg | Lys | Lys | Gly | Asp | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gln | Pro | Val | Asn | Gln | Leu | Cys | Gln | Met | Leu | Gly | Lys | Ile | Ile | Ala | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Asn | Gln | Ser | Arg | Gly | Lys | Gly | Pro | Gly | Lys | Lys | Asn | Lys | Lys | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Pro | Glu | Lys | Pro | His | Phe | Pro | Leu | Ala | Thr | Glu | Asp | Asp | Val | Arg |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | His | Phe | Thr | Pro | Ser | Glu | Arg | Gln | Leu | Cys | Leu | Ser | Ser | Ile | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Thr | Ala | Phe | Asn | Gln | Gly | Ala | Gly | Thr | Cys | Thr | Leu | Ser | Asp | Ser | Gly |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Ile | Ser | Tyr | Thr | Val | Glu | Phe | Ser | Leu | Pro | Thr | His | His | Thr | Val |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Arg | Leu | Ile | Arg | Val | Thr | Ala | Ser | Pro | Ser | Ala |     |     |     |     |     |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

|   |     |
|---|-----|
| ATG CCA AAT AAC AAC GGT AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC | 48  |
| Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly |     |
| 1 5 10 15   |     |
| CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGC AAG ATC ATC GCT CAG | 96  |
| Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln |     |
| 20 25 30  |     |
| CAA AAT CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA | 144 |
| Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys |     |
| 35 40 45  |     |
| AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA | 192 |
| Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg |     |
| 50 55 60  |     |
| CAT CAC TTT ACC CCT AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG | 240 |
| His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln |     |
| 65 70 75 80   |     |
| ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG | 288 |
| Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly |     |
| 85 90 95  |     |
| AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCT ACG CAT CAT ACT GTG | 336 |
| Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val |     |
| 100 105 110   |     |
| CGC CTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA                 | 372 |
| Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala                     |     |
| 115 120   |     |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Asn | Asn | Asn | Gly | Lys | Gln | Gln | Lys | Arg | Lys | Lys | Gly | Asp | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gln | Pro | Val | Asn | Gln | Leu | Cys | Gln | Met | Leu | Gly | Lys | Ile | Ile | Ala | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Asn | Gln | Ser | Arg | Gly | Lys | Gly | Pro | Gly | Lys | Lys | Asn | Lys | Lys | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Pro | Glu | Lys | Pro | His | Phe | Pro | Leu | Ala | Thr | Glu | Asp | Asp | Val | Arg |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | His | Phe | Thr | Pro | Ser | Glu | Arg | Gln | Leu | Cys | Leu | Ser | Ser | Ile | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Thr | Ala | Phe | Asn | Gln | Gly | Ala | Gly | Thr | Cys | Thr | Leu | Ser | Asp | Ser | Gly |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Ile | Ser | Tyr | Thr | Val | Glu | Phe | Ser | Leu | Pro | Thr | His | His | Thr | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Arg | Leu | Ile | Arg | Val | Thr | Ala | Ser | Pro | Ser | Ala |     |     |     |     |     |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | CCA | AAT | AAC | AAC | GGC | AAG | CAG | CAG | AAG | AGA | AAG | AAG | GGG | GAT | GGC | 48  |
| Met | Pro | Asn | Asn | Asn | Gly | Lys | Gln | Gln | Lys | Arg | Lys | Lys | Gly | Asp | Gly |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CAG | CCA | GTC | AAT | CAG | CTG | TGC | CAG | ATG | CTG | GGT | AAG | ATC | ATC | GCC | CAG | 96  |
| Gln | Pro | Val | Asn | Gln | Leu | Cys | Gln | Met | Leu | Gly | Lys | Ile | Ile | Ala | Gln |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CAA | AAC | CAG | TCT | AGA | GGC | AAG | GGA | CCG | GGA | AAG | AAA | AAT | AAG | AAG | AAA | 144 |
| Gln | Asn | Gln | Ser | Arg | Gly | Lys | Gly | Pro | Gly | Lys | Lys | Asn | Lys | Lys | Lys |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| AAC | CCG | GAG | AAG | CCC | CAT | TTT | CCT | CTA | GCG | ACT | GAA | GAT | GAT | GTC | AGA | 192 |
| Asn | Pro | Glu | Lys | Pro | His | Phe | Pro | Leu | Ala | Thr | Glu | Asp | Asp | Val | Arg |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CAT | CAC | TTT | ACC | CCT | AGT | GAG | CGG | CAA | TTG | TGT | CTG | TCG | TCA | ATC | CAA | 240 |
| His | His | Phe | Thr | Pro | Ser | Glu | Arg | Gln | Leu | Cys | Leu | Ser | Ser | Ile | Gln |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| ACT | GCC | TTT | AAT | CAA | GGC | GCT | GGG | ACT | TGC | ACC | CTG | TCA | GAT | TCA | GGG | 288 |
| Thr | Ala | Phe | Asn | Gln | Gly | Ala | Gly | Thr | Cys | Thr | Leu | Ser | Asp | Ser | Gly |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| AGG | ATA | AGT | TAC | ACT | GTG | GAG | TTT | AGT | TTG | CCT | ACG | CAT | CAT | ACT | GTG | 336 |
| Arg | Ile | Ser | Tyr | Thr | Val | Glu | Phe | Ser | Leu | Pro | Thr | His | His | Thr | Val |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| CGC | TTG | ATC | CGC | GTC | ACA | GCA | TCA | CCC | TCA | GCA | TGA |     |     |     |     | 372 |
| Arg | Leu | Ile | Arg | Val | Thr | Ala | Ser | Pro | Ser | Ala |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Asn | Asn | Asn | Gly | Lys | Gln | Gln | Lys | Arg | Lys | Lys | Gly | Asp | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gln | Pro | Val | Asn | Gln | Leu | Cys | Gln | Met | Leu | Gly | Lys | Ile | Ile | Ala | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |

Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys  
 35 40 45  
 Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg  
 50 55 60  
 His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln  
 65 70 75 80  
 Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly  
 85 90 95  
 Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val  
 100 105 110  
 Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala  
 115 120

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|   |    |
|---|----|
| ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AAA AAG AAG GGG GAT GGC | 48 |
| Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly |    |
| 1 5 10 15   |    |
| CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAG | 96 |
| Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln |    |
| 20 25 30  |    |

|   |     |
|---|-----|
| CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAC AAG AAG AAA | 144 |
| Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys |     |
| 35 40 45  |     |
| AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA | 192 |
| Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg |     |
| 50 55 60  |     |
| CAT CAC TTC ACC TCT GGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG | 240 |
| His His Phe Thr Ser Gly Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln |     |
| 65 70 75 80   |     |
| ACA GCC TTT AAT CAA GGC GCT GGA ACT TGT ACC CTG TCA GAT TCA GGG | 288 |
| Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly |     |
| 85 90 95  |     |
| AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCG ACG CAT CAT ACT GTG | 336 |
| Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val |     |
| 100 105 110   |     |
| CGC TTG ATC CGC GTC ACA GCG TCA CCC TCA GCA TGA                 | 372 |
| Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala                     |     |
| 115 120   |     |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|   |  |
|---|--|
| Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly |  |
| 1 5 10 15   |  |
| Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln |  |
| 20 25 30  |  |
| Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys |  |
| 35 40 45  |  |
| Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg |  |
| 50 55 60  |  |
| His His Phe Thr Ser Gly Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln |  |
| 65 70 75 80   |  |



Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly  
85 90 95  
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val  
100 105 110  
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|   |     |
|---|-----|
| ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AAA AAG AAG GGG GAT GGC | 48  |
| Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly |     |
| 1 5 10 15   |     |
| CAG CCA GTC AAT CAG CTC TGC CAA ATG CTG GGT AAG ATC ATC GCC CAG | 96  |
| Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln |     |
| 20 25 30  |     |
| CAA AAC CAG TCC AGA GGT AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA | 144 |
| Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys |     |
| 35 40 45  |     |
| AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA | 192 |
| Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| CAT CAC TTC ACC CCC AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG | 240 |
| His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln |     |
| 65 70 75 80   |     |
| ACT GCC TTT AAT CAG GGC GCT GGG ACC TGT ATC CTA TCA GAT TCA GGG | 288 |
| Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Ile Leu Ser Asp Ser Gly |     |
| 85 90 95  |     |
| AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCG ACG CAT CAT ACT GTG | 336 |
| Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val |     |
| 100 105 110   |     |
| CGC CTG ATT CGC GTC ACG GCA CCA CCC TCA GCA TGA                 | 372 |
| Arg Leu Ile Arg Val Thr Ala Pro Pro Ser Ala                     |     |
| 115 120   |     |

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|   |  |
|---|--|
| Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly |  |
| 1 5 10 15   |  |
| Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln |  |
| 20 25 30  |  |
| Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys |  |
| 35 40 45  |  |
| Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg |  |
| 50 55 60  |  |
| His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln |  |
| 65 70 75 80   |  |
| Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Ile Leu Ser Asp Ser Gly |  |
| 85 90 95  |  |
| Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val |  |
| 100 105 110   |  |
| Arg Leu Ile Arg Val Thr Ala Pro Pro Ser Ala                     |  |
| 115 120   |  |

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Lys Lys Ser Thr Ala Pro Met  
1 5

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Ser Gln Gly  
1

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 240 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;  
(A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

|   |     |
|---|-----|
| TCTTCTTGCC TTTTCTATGC TTCTGAGATG AGTGAAAAGG GATTTAAGGT GGTATTTGGC | 60  |
| AATGTGTCAG GCATCGTGGC AGTGTGCGTC AACTTCACCA GTTACGTCCA ACATGTCAAG | 120 |
| GAATTTACCC AACGTTCTT GGTAGTTGAC CATGTGCGGC TGCTCCATTT CATGACGCCC  | 180 |
| GAGACCATGA GGTGGGCAAC TGTTTTAGCC TGTCTTTTTA CCATTCTGTT GGCAATTGA  | 240 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|   |     |
|---|-----|
| CCTGAATTGA GATGAAATGG GGTCTATGCA AAGCCTTTTT GACAAAATTG GCCAACTTTT | 60  |
| TGTGGATGCT TTCACGGAGT TCTTGGTGTC CATTGTTGAT ATCATTATAT TTTTGGCCAT | 120 |
| TTTGTTTGGC TTCACCATCG CAGGTTGGCT GGTGGTCTTT TGCATCAGAT TGGTTTGCTC | 180 |
| CGCGATACTC CGTGCGCGCC CTGCCATTCA CTCTGAGCAA TTACAGAAGA TCCTATGAGG | 240 |
| CCTTTCTCTC TCAGTGCCAG GTGGACATTC CCACCTGGGG AACTAAACAT CCTTTGGGGA | 300 |
| TGCTTTGGCA CCATAAGGTG TCAACCCTGA TTGATGAAAT GGTGTCGCGT CGAATGTACC | 360 |
| GCATCATGGA AAAAGCAGGA CAGGCTGCCT GGAAACAGGT AGTGAGCGAG GCTACGCTGT | 420 |
| CTCGCATTAG TAGTTTGGAT GTGGTGGCTC ATTTTCAGCA TCTTGCCGCC ATTGAAGCCG | 480 |
| AGACCTGTAA ATATCTGGCC TCTCGGCTGC CCATGCTACA CCACCTGCGC ATGACAGGGT | 540 |
| CAAATGTAAC CATAGTGTAT AATAGTACTT TGAATCAGGT GTTTGCTGTT TTCCCAACCC | 600 |
| CTGGTTCCCG GCCAAAGCTT CATGATTTCC AGCAATGGCT AATAGCTGTA CATTCCTCTA | 660 |

|  |      |
|--|------|
| TATTTTCCTC TGTTCAGCT TCTTGACTC TTTTGTGTG GCTGTGGTTG CGGGTTCCAA     | 720  |
| TGCTACGTAC TGTTTTTGGT TTCCGCTGGT TAGGGGCAAT TTTTCTTTTCG AACTCACGGT | 780  |
| GAATTACACG GTGTGCCCCG CTTGCCTCAC CCGGCAAGCA GCCGCAGAGG CCTACGAACC  | 840  |
| CGGCAGGTCC CTTTGGTGCA GGATAGGGCA TGATCGATGT GGGGAGGACG ATCATGATGA  | 900  |
| ACTAGGGTTT TGGGTGCCGT CTGGCCTCTC CAGCGAAGGC CACTTGACCA GTGCTTACGC  | 960  |
| CTGGTTGGCG TCCCTGTCCT TCAGCTATAC GGCCCAGTTC CATCCCGAGA TATTCGGGAT  | 1020 |
| AGGGAATGTG AGTCGAGTCT ATGTTGACAT CAAGCACCAA TTCATTGCG CTGTTTCATGA  | 1080 |
| TGGGCAGAAC ACCACCTTGC CCCACCATGA CAACATTTC GCGTGCTTC AGACCTATTA    | 1140 |
| CCAGCATCAG GTCGACGGGG GCAATTGGTT TCACCTAGAA TGGGTGCGTC CCTTCTTTTC  | 1200 |
| CTCTTGGTTG GTTTTAAATG TCTCTTGGTT TCTCAGGCGT TCGCCTGCAA GCCATGTTTC  | 1260 |
| AGTTCGAGTC TTTCAGACAT CAAGACCAAC ACCACCGCAG CGGCAGGCTT TGCTGTCCTC  | 1320 |
| CAAGACATCA GTTGCCTTAG GCATCGCAAC TCGGCCTCTG AGGCGATTTCG CAAAGTCCCT | 1380 |
| CAGTGCCGCA CGGCGATAGG GACACCCGTG TATATCACTG TCACAGCCAA TGTTACCGAT  | 1440 |
| GAGAATTATT TGCATTCCTC TGATCTTCTC ATGCTTTCTT CTTGCCTTTT CTATGCTTCT  | 1500 |
| GAGATGAGTG AAAAGGGATT TAAGGTGGTA TTTGGCAATG TGTCAGGCAT CGTGGCAGTG  | 1560 |
| TGCGTCAACT TCACCAGTTA CGTCCAACAT GTCAAGGAAT TTACCCAACG TTCCTTGGTA  | 1620 |
| GTTGACCATG TCGGGCTGCT CCATTTCATG ACGCCCGAGA CCATGAGGTG GGCAACTGTT  | 1680 |
| TTAGCCTGTC TTTTACCAT TCTGTTGGCA ATTTGAATGT TTAAGTATGT TGGGGAAATG   | 1740 |
| CTTGACCGCG GGCTGTTGCT CGCAATTGCT TTTTTTATGG TGTATCGTGC CGTCTTGTT   | 1799 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|   |     |
|---|-----|
| ATG AAA TGG GGT CTA TGC AAA GCC TTT TTG ACA AAA TTG GCC AAC TTT | 48  |
| Met Lys Trp Gly Leu Cys Lys Ala Phe Leu Thr Lys Leu Ala Asn Phe |     |
| 1 5 10 15   |     |
| TTG TGG ATG CTT TCA CGG AGT TCT TGG TGT CCA TTG TTG ATA TCA TTA | 96  |
| Leu Trp Met Leu Ser Arg Ser Ser Trp Cys Pro Leu Leu Ile Ser Leu |     |
| 20 25 30  |     |
| TAT TTT TGG CCA TTT TGT TTG GCT TCA CCA TCG CAG GTT GGC TGG TGG | 144 |
| Tyr Phe Trp Pro Phe Cys Leu Ala Ser Pro Ser Gln Val Gly Trp Trp |     |
| 35 40 45  |     |
| TCT TTT GCA TCA GAT TGG TTT GCT CCG CGA TAC TCC GTG CGC GCC CTG | 192 |
| Ser Phe Ala Ser Asp Trp Phe Ala Pro Arg Tyr Ser Val Arg Ala Leu |     |
| 50 55 60  |     |
| CCA TTC ACT CTG AGC AAT TAC AGA AGA TCC TAT GAG GCC TTT CTC TCT | 240 |
| Pro Phe Thr Leu Ser Asn Tyr Arg Arg Ser Tyr Glu Ala Phe Leu Ser |     |
| 65 70 75 80   |     |
| CAG TGC CAG GTG GAC ATT CCC ACC TGG GGA ACT AAA CAT CCT TTG GGG | 288 |
| Gln Cys Gln Val Asp Ile Pro Thr Trp Gly Thr Lys His Pro Leu Gly |     |
| 85 90 95  |     |
| ATG CTT TGG CAC CAT AAG GTG TCA ACC CTG ATT GAT GAA ATG GTG TCG | 336 |
| Met Leu Trp His His Lys Val Ser Thr Leu Ile Asp Glu Met Val Ser |     |
| 100 105 110   |     |
| CGT CGA ATG TAC CGC ATC ATG GAA AAA GCA GGA CAG GCT GCC TGG AAA | 384 |
| Arg Arg Met Tyr Arg Ile Met Glu Lys Ala Gly Gln Ala Ala Trp Lys |     |
| 115 120 125   |     |
| CAG GTA GTG AGC GAG GCT ACG CTG TCT CGC ATT AGT AGT TTG GAT GTG | 432 |
| Gln Val Val Ser Glu Ala Thr Leu Ser Arg Ile Ser Ser Leu Asp Val |     |
| 130 135 140   |     |
| GTG GCT CAT TTT CAG CAT CTT GCC GCC ATT GAA GCC GAG ACC TGT AAA | 480 |
| Val Ala His Phe Gln His Leu Ala Ala Ile Glu Ala Glu Thr Cys Lys |     |
| 145 150 155 160   |     |

|   |     |
|---|-----|
| TAT CTG GCC TCT CGG CTG CCC ATG CTA CAC CAC CTG CGC ATG ACA GGG | 528 |
| Tyr Leu Ala Ser Arg Leu Pro Met Leu His His Leu Arg Met Thr Gly |     |
| 165 170 175   |     |
| TCA AAT GTA ACC ATA GTG TAT AAT AGT ACT TTG AAT CAG GTG TTT GCT | 576 |
| Ser Asn Val Thr Ile Val Tyr Asn Ser Thr Leu Asn Gln Val Phe Ala |     |
| 180 185 190   |     |
| GTT TTC CCA ACC CCT GGT TCC CGG CCA AAG CTT CAT GAT TTC CAG CAA | 624 |
| Val Phe Pro Thr Pro Gly Ser Arg Pro Lys Leu His Asp Phe Gln Gln |     |
| 195 200 205   |     |
| TGG CTA ATA GCT GTA CAT TCC TCT ATA TTT TCC TCT GTT GCA GCT TCT | 672 |
| Trp Leu Ile Ala Val His Ser Ser Ile Phe Ser Ser Val Ala Ala Ser |     |
| 210 215 220   |     |
| TGT ACT CTT TTT GTT GTG CTG TGG TTG CGG GTT CCA ATG CTA CGT ACT | 720 |
| Cys Thr Leu Phe Val Val Leu Trp Leu Arg Val Pro Met Leu Arg Thr |     |
| 225 230 235 240   |     |
| GTT TTT GGT TTC CGC TGG TTA GGG GCA ATT TTT CTT TCG AAC TCA CGG | 768 |
| Val Phe Gly Phe Arg Trp Leu Gly Ala Ile Phe Leu Ser Asn Ser Arg |     |
| 245 250 255   |     |
| TGA   | 771 |

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Trp | Gly | Leu | Cys | Lys | Ala | Phe | Leu | Thr | Lys | Leu | Ala | Asn | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Trp | Met | Leu | Ser | Arg | Ser | Ser | Trp | Cys | Pro | Leu | Leu | Ile | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Phe | Trp | Pro | Phe | Cys | Leu | Ala | Ser | Pro | Ser | Gln | Val | Gly | Trp | Trp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Ala | Ser | Asp | Trp | Phe | Ala | Pro | Arg | Tyr | Ser | Val | Arg | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Phe | Thr | Leu | Ser | Asn | Tyr | Arg | Arg | Ser | Tyr | Glu | Ala | Phe | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Cys | Gln | Val | Asp | Ile | Pro | Thr | Trp | Gly | Thr | Lys | His | Pro | Leu | Gly | 85  | 90  | 95  |
| Met | Leu | Trp | His | His | Lys | Val | Ser | Thr | Leu | Ile | Asp | Glu | Met | Val | Ser | 100 | 105 | 110 |
| Arg | Arg | Met | Tyr | Arg | Ile | Met | Glu | Lys | Ala | Gly | Gln | Ala | Ala | Trp | Lys | 115 | 120 | 125 |
| Gln | Val | Val | Ser | Glu | Ala | Thr | Leu | Ser | Arg | Ile | Ser | Ser | Leu | Asp | Val | 130 | 135 | 140 |
| Val | Ala | His | Phe | Gln | His | Leu | Ala | Ala | Ile | Glu | Ala | Glu | Thr | Cys | Lys | 145 | 150 | 155 |
| Tyr | Leu | Ala | Ser | Arg | Leu | Pro | Met | Leu | His | His | Leu | Arg | Met | Thr | Gly | 165 | 170 | 175 |
| Ser | Asn | Val | Thr | Ile | Val | Tyr | Asn | Ser | Thr | Leu | Asn | Gln | Val | Phe | Ala | 180 | 185 | 190 |
| Val | Phe | Pro | Thr | Pro | Gly | Ser | Arg | Pro | Lys | Leu | His | Asp | Phe | Gln | Gln | 195 | 200 | 205 |
| Trp | Leu | Ile | Ala | Val | His | Ser | Ser | Ile | Phe | Ser | Ser | Val | Ala | Ala | Ser | 210 | 215 | 220 |
| Cys | Thr | Leu | Phe | Val | Val | Leu | Trp | Leu | Arg | Val | Pro | Met | Leu | Arg | Thr | 225 | 230 | 235 |
| Val | Phe | Gly | Phe | Arg | Trp | Leu | Gly | Ala | Ile | Phe | Leu | Ser | Asn | Ser | Arg | 245 | 250 | 255 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS



(B) LOCATION: 1..762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

|   |     |
|---|-----|
| ATG GCT AAT AGC TGT ACA TTC CTC TAT ATT TTC CTC TGT TGC AGC TTC | 48  |
| Met Ala Asn Ser Cys Thr Phe Leu Tyr Ile Phe Leu Cys Cys Ser Phe |     |
| 1 5 10 15   |     |
| TTG TAC TCT TTT TGT TGT GCT GTG GTT GCG GGT TCC AAT GCT ACG TAC | 96  |
| Leu Tyr Ser Phe Cys Cys Ala Val Val Ala Gly Ser Asn Ala Thr Tyr |     |
| 20 25 30  |     |
| TGT TTT TGG TTT CCG CTG GTT AGG GGC AAT TTT TCT TTC GAA CTC ACG | 144 |
| Cys Phe Trp Phe Pro Leu Val Arg Gly Asn Phe Ser Phe Glu Leu Thr |     |
| 35 40 45  |     |
| GTG AAT TAC ACG GTG TGC CCG CCT TGC CTC ACC CGG CAA GCA GCC GCA | 192 |
| Val Asn Tyr Thr Val Cys Pro Pro Cys Leu Thr Arg Gln Ala Ala Ala |     |
| 50 55 60  |     |
| GAG GCC TAC GAA CCC GGC AGG TCC CTT TGG TGC AGG ATA GGG CAT GAT | 240 |
| Glu Ala Tyr Glu Pro Gly Arg Ser Leu Trp Cys Arg Ile Gly His Asp |     |
| 65 70 75 80   |     |
| CGA TGT GGG GAG GAC GAT CAT GAT GAA CTA GGG TTT GTG GTG CCG TCT | 288 |
| Arg Cys Gly Glu Asp Asp His Asp Glu Leu Gly Phe Val Val Pro Ser |     |
| 85 90 95  |     |
| GGC CTC TCC AGC GAA GGC CAC TTG ACC AGT GCT TAC GCC TGG TTG GCG | 336 |
| Gly Leu Ser Ser Glu Gly His Leu Thr Ser Ala Tyr Ala Trp Leu Ala |     |
| 100 105 110   |     |
| TCC CTG TCC TTC AGC TAT ACG GCC CAG TTC CAT CCC GAG ATA TTC GGG | 384 |
| Ser Leu Ser Phe Ser Tyr Thr Ala Gln Phe His Pro Glu Ile Phe Gly |     |
| 115 120 125   |     |
| ATA GGG AAT GTG AGT CGA GTC TAT GTT GAC ATC AAG CAC CAA TTC ATT | 432 |
| Ile Gly Asn Val Ser Arg Val Tyr Val Asp Ile Lys His Gln Phe Ile |     |
| 130 135 140   |     |
| TGC GCT GTT CAT GAT GGG CAG AAC ACC ACC TTG CCC CAC CAT GAC AAC | 480 |
| Cys Ala Val His Asp Gly Gln Asn Thr Thr Leu Pro His His Asp Asn |     |
| 145 150 155 160   |     |
| ATT TCA GCC GTG CTT CAG ACC TAT TAC CAG CAT CAG GTC GAC GGG GGC | 528 |
| Ile Ser Ala Val Leu Gln Thr Tyr Tyr Gln His Gln Val Asp Gly Gly |     |
| 165 170 175   |     |
| AAT TGG TTT CAC CTA GAA TGG GTG CGT CCC TTC TTT TCC TCT TGG TTG | 576 |
| Asn Trp Phe His Leu Glu Trp Val Arg Pro Phe Phe Ser Ser Trp Leu |     |
| 180 185 190   |     |

|   |     |
|---|-----|
| GTT TTA AAT GTC TCT TGG TTT CTC AGG CGT TCG CCT GCA AGC CAT GTT | 624 |
| Val Leu Asn Val Ser Trp Phe Leu Arg Arg Ser Pro Ala Ser His Val |     |
| 195 200 205   |     |
| TCA GTT CGA GTC TTT CAG ACA TCA AGA CCA ACA CCA CCG CAG CGG CAG | 672 |
| Ser Val Arg Val Phe Gln Thr Ser Arg Pro Thr Pro Pro Gln Arg Gln |     |
| 210 215 220   |     |
| GCT TTG CTG TCC TCC AAG ACA TCA GTT GCC TTA GGC ATC GCA ACT CGG | 720 |
| Ala Leu Leu Ser Ser Lys Thr Ser Val Ala Leu Gly Ile Ala Thr Arg |     |
| 225 230 235 240   |     |
| CCT CTG AGG CGA TTC GCA AAG TCC CTC AGT GCC GCA CGG CGA         | 762 |
| Pro Leu Arg Arg Phe Ala Lys Ser Leu Ser Ala Ala Arg Arg         |     |
| 245 250   |     |
| TAG   | 765 |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Asn | Ser | Cys | Thr | Phe | Leu | Tyr | Ile | Phe | Leu | Cys | Cys | Ser | Phe | 1   | 5   | 10  | 15 |
| Leu | Tyr | Ser | Phe | Cys | Cys | Ala | Val | Val | Ala | Gly | Ser | Asn | Ala | Thr | Tyr | 20  | 25  | 30  |    |
| Cys | Phe | Trp | Phe | Pro | Leu | Val | Arg | Gly | Asn | Phe | Ser | Phe | Glu | Leu | Thr | 35  | 40  | 45  |    |
| Val | Asn | Tyr | Thr | Val | Cys | Pro | Pro | Cys | Leu | Thr | Arg | Gln | Ala | Ala | Ala | 50  | 55  | 60  |    |
| Glu | Ala | Tyr | Glu | Pro | Gly | Arg | Ser | Leu | Trp | Cys | Arg | Ile | Gly | His | Asp | 65  | 70  | 75  | 80 |
| Arg | Cys | Gly | Glu | Asp | Asp | His | Asp | Glu | Leu | Gly | Phe | Val | Val | Pro | Ser | 85  | 90  | 95  |    |
| Gly | Leu | Ser | Ser | Glu | Gly | His | Leu | Thr | Ser | Ala | Tyr | Ala | Trp | Leu | Ala | 100 | 105 | 110 |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Ser | Phe | Ser | Tyr | Thr | Ala | Gln | Phe | His | Pro | Glu | Ile | Phe | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Gly | Asn | Val | Ser | Arg | Val | Tyr | Val | Asp | Ile | Lys | His | Gln | Phe | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Ala | Val | His | Asp | Gly | Gln | Asn | Thr | Thr | Leu | Pro | His | His | Asp | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Ser | Ala | Val | Leu | Gln | Thr | Tyr | Tyr | Gln | His | Gln | Val | Asp | Gly | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Trp | Phe | His | Leu | Glu | Trp | Val | Arg | Pro | Phe | Phe | Ser | Ser | Trp | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Leu | Asn | Val | Ser | Trp | Phe | Leu | Arg | Arg | Ser | Pro | Ala | Ser | His | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Val | Arg | Val | Phe | Gln | Thr | Ser | Arg | Pro | Thr | Pro | Pro | Gln | Arg | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Leu | Leu | Ser | Ser | Lys | Thr | Ser | Val | Ala | Leu | Gly | Ile | Ala | Thr | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Leu | Arg | Arg | Phe | Ala | Lys | Ser | Leu | Ser | Ala | Ala | Arg | Arg |     |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|   |     |
|---|-----|
| ATG GGT GCG TCC CTT CTT TTC CTC TTG GTT GGT TTT AAA TGT CTC TTG | 48  |
| Met Gly Ala Ser Leu Leu Phe Leu Leu Val Gly Phe Lys Cys Leu Leu |     |
| 1 5 10 15   |     |
| GTT TCT CAG GCG TTC GCC TGC AAG CCA TGT TTC AGT TCG AGT CTT TCA | 96  |
| Val Ser Gln Ala Phe Ala Cys Lys Pro Cys Phe Ser Ser Ser Leu Ser |     |
| 20 25 30  |     |
| GAC ATC AAG ACC AAC ACC ACC GCA GCG GCA GGC TTT GCT GTC CTC CAA | 144 |
| Asp Ile Lys Thr Asn Thr Thr Ala Ala Ala Gly Phe Ala Val Leu Gln |     |
| 35 40 45  |     |
| GAC ATC AGT TGC CTT AGG CAT CGC AAC TCG GCC TCT GAG GCG ATT CGC | 192 |
| Asp Ile Ser Cys Leu Arg His Arg Asn Ser Ala Ser Glu Ala Ile Arg |     |
| 50 55 60  |     |
| AAA GTC CCT CAG TGC CGC ACG GCG ATA GGG ACA CCC GTG TAT ATC ACT | 240 |
| Lys Val Pro Gln Cys Arg Thr Ala Ile Gly Thr Pro Val Tyr Ile Thr |     |
| 65 70 75 80   |     |
| GTC ACA GCC AAT GTT ACC GAT GAG AAT TAT TTG CAT TCC TCT GAT CTT | 288 |
| Val Thr Ala Asn Val Thr Asp Glu Asn Tyr Leu His Ser Ser Asp Leu |     |
| 85 90 95  |     |
| CTC ATG CTT TCT TCT TGC CTT TTC TAT GCT TCT GAG ATG AGT GAA AAG | 336 |
| Leu Met Leu Ser Ser Cys Leu Phe Tyr Ala Ser Glu Met Ser Glu Lys |     |
| 100 105 110   |     |
| GGA TTT AAG GTG GTA TTT GGC AAT GTG TCA GGC ATC GTG GCA GTG TGC | 384 |
| Gly Phe Lys Val Val Phe Gly Asn Val Ser Gly Ile Val Ala Val Cys |     |
| 115 120 125   |     |
| GTC AAC TTC ACC AGT TAC GTC CAA CAT GTC AAG GAA TTT ACC CAA CGT | 432 |
| Val Asn Phe Thr Ser Tyr Val Gln His Val Lys Glu Phe Thr Gln Arg |     |
| 130 135 140   |     |
| TCC TTG GTA GTT GAC CAT GTG CGG CTG CTC CAT TTC ATG ACG CCC GAG | 480 |
| Ser Leu Val Val Asp His Val Arg Leu Leu His Phe Met Thr Pro Glu |     |
| 145 150 155 160   |     |
| ACC ATG AGG TGG GCA ACT GTT TTA GCC TGT CTT TTT ACC ATT CTG TTG | 528 |
| Thr Met Arg Trp Ala Thr Val Leu Ala Cys Leu Phe Thr Ile Leu Leu |     |
| 165 170 175   |     |
| GCA ATT TGA   | 537 |
| Ala Ile   |     |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ala | Ser | Leu | Leu | Phe | Leu | Leu | Val | Gly | Phe | Lys | Cys | Leu | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Ser | Gln | Ala | Phe | Ala | Cys | Lys | Pro | Cys | Phe | Ser | Ser | Ser | Leu | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Ile | Lys | Thr | Asn | Thr | Thr | Ala | Ala | Ala | Gly | Phe | Ala | Val | Leu | Gln |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Ile | Ser | Cys | Leu | Arg | His | Arg | Asn | Ser | Ala | Ser | Glu | Ala | Ile | Arg |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Val | Pro | Gln | Cys | Arg | Thr | Ala | Ile | Gly | Thr | Pro | Val | Tyr | Ile | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Val | Thr | Ala | Asn | Val | Thr | Asp | Glu | Asn | Tyr | Leu | His | Ser | Ser | Asp | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Met | Leu | Ser | Ser | Cys | Leu | Phe | Tyr | Ala | Ser | Glu | Met | Ser | Glu | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Phe | Lys | Val | Val | Phe | Gly | Asn | Val | Ser | Gly | Ile | Val | Ala | Val | Cys |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Asn | Phe | Thr | Ser | Tyr | Val | Gln | His | Val | Lys | Glu | Phe | Thr | Gln | Arg |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ser | Leu | Val | Val | Asp | His | Val | Arg | Leu | Leu | His | Phe | Met | Thr | Pro | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr | Met | Arg | Trp | Ala | Thr | Val | Leu | Ala | Cys | Leu | Phe | Thr | Ile | Leu | Leu |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ala | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus

(C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|   |     |
|---|-----|
| ATG CAA TGG GGT CAC TGT GGA GTA AAA TCA GCC AGC TGT TCG TGG ACG | 48  |
| Met Gln Trp Gly His Cys Gly Val Lys Ser Ala Ser Cys Ser Trp Thr |     |
| 1 5 10 15   |     |
| CCT TCA CTG AGT TCC TTG TTA GTG TGG TTG ATA TTG CCA TTT TCC TTG | 96  |
| Pro Ser Leu Ser Ser Leu Leu Val Trp Leu Ile Leu Pro Phe Ser Leu |     |
| 20 25 30  |     |
| CCA TAC TGT TTG GGT TCA CCG TCG CAG GAT GGT TAC TGG TCT TTC TTC | 144 |
| Pro Tyr Cys Leu Gly Ser Pro Ser Gln Asp Gly Tyr Trp Ser Phe Phe |     |
| 35 40 45  |     |
| TCA GAG TGG TTT GCT CCG CGC TTC TCC GTT CGC GCT CTG CCA TTC ACT | 192 |
| Ser Glu Trp Phe Ala Pro Arg Phe Ser Val Arg Ala Leu Pro Phe Thr |     |
| 50 55 60  |     |
| CTC CCG AAC TAT CGA AGG TCC TAT GAA GGC TTG TTG CCC AAC TGC AGA | 240 |
| Leu Pro Asn Tyr Arg Arg Ser Tyr Glu Gly Leu Leu Pro Asn Cys Arg |     |
| 65 70 75 80   |     |
| CCG GAT GTC CCA CAA TTT GCA GTC AAG CAC CCA TTG GGT ATG TTT TGG | 288 |
| Pro Asp Val Pro Gln Phe Ala Val Lys His Pro Leu Gly Met Phe Trp |     |
| 85 90 95  |     |
| CAC ATG CGA GTT TCC CAC TTG ATT GAT GAG ATG GTC TCT CGT CGC ATT | 336 |
| His Met Arg Val Ser His Leu Ile Asp Glu Met Val Ser Arg Arg Ile |     |
| 100 105 110   |     |
| TAC CAG ACC ATG GAA CAT TCA GGT CAA GCG GCC TGG AAG CAG GTG GTT | 384 |
| Tyr Gln Thr Met Glu His Ser Gly Gln Ala Ala Trp Lys Gln Val Val |     |
| 115 120 125   |     |
| GGT GAG GCC ACT CTC ACG AAG CTG TCA GGG CTC GAT ATA GTT ACT CAT | 432 |
| Gly Glu Ala Thr Leu Thr Lys Leu Ser Gly Leu Asp Ile Val Thr His |     |
| 130 135 140   |     |

|   |     |
|---|-----|
| TTC CAA CAC CTG GCC GCA GTG GAG GCG GAT TCT TGC CGC TTT CTC AGC | 480 |
| Phe Gln His Leu Ala Ala Val Glu Ala Asp Ser Cys Arg Phe Leu Ser |     |
| 145 150 155 160   |     |
| TCA CGA CTC GTG ATG CTA AAA AAT CTT GCC GTT GGC AAT GTG AGC CTA | 528 |
| Ser Arg Leu Val Met Leu Lys Asn Leu Ala Val Gly Asn Val Ser Leu |     |
| 165 170 175   |     |
| CAG TAC AAC ACC ACG TTG GAC CGC GTT GAG CTC ATC TTC CCC ACG CCA | 576 |
| Gln Tyr Asn Thr Thr Leu Asp Arg Val Glu Leu Ile Phe Pro Thr Pro |     |
| 180 185 190   |     |
| GGT ACG AGG CCC AAG TTG ACC GAT TTC AGA CAA TGG CTC ATC AGT GTG | 624 |
| Gly Thr Arg Pro Lys Leu Thr Asp Phe Arg Gln Trp Leu Ile Ser Val |     |
| 195 200 205   |     |
| CAC GCT TCC ATT TTT TCC TCT GTG GCT TCA TCT GTT ACC TTG TTC ATA | 672 |
| His Ala Ser Ile Phe Ser Ser Val Ala Ser Ser Val Thr Leu Phe Ile |     |
| 210 215 220   |     |
| GTG CTT TGG CTT CGA ATT CCA GCT CTA CGC TAT GTT TTT GGT TTC CAT | 720 |
| Val Leu Trp Leu Arg Ile Pro Ala Leu Arg Tyr Val Phe Gly Phe His |     |
| 225 230 235 240   |     |
| TGG CCC ACG GCA ACA CAT CAT TCG AGC TGA                         | 750 |
| Trp Pro Thr Ala Thr His His Ser Ser                             |     |
| 245   |     |

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|   |  |
|---|--|
| Met Gln Trp Gly His Cys Gly Val Lys Ser Ala Ser Cys Ser Trp Thr |  |
| 1 5 10 15   |  |
| Pro Ser Leu Ser Ser Leu Leu Val Trp Leu Ile Leu Pro Phe Ser Leu |  |
| 20 25 30  |  |
| Pro Tyr Cys Leu Gly Ser Pro Ser Gln Asp Gly Tyr Trp Ser Phe Phe |  |
| 35 40 45  |  |
| Ser Glu Trp Phe Ala Pro Arg Phe Ser Val Arg Ala Leu Pro Phe Thr |  |
| 50 55 60  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Asn | Tyr | Arg | Arg | Ser | Tyr | Glu | Gly | Leu | Leu | Pro | Asn | Cys | Arg | 65  | 70  | 75  | 80  |
| Pro | Asp | Val | Pro | Gln | Phe | Ala | Val | Lys | His | Pro | Leu | Gly | Met | Phe | Trp | 85  | 90  | 95  |     |
| His | Met | Arg | Val | Ser | His | Leu | Ile | Asp | Glu | Met | Val | Ser | Arg | Arg | Ile | 100 | 105 | 110 |     |
| Tyr | Gln | Thr | Met | Glu | His | Ser | Gly | Gln | Ala | Ala | Trp | Lys | Gln | Val | Val | 115 | 120 | 125 |     |
| Gly | Glu | Ala | Thr | Leu | Thr | Lys | Leu | Ser | Gly | Leu | Asp | Ile | Val | Thr | His | 130 | 135 | 140 |     |
| Phe | Gln | His | Leu | Ala | Ala | Val | Glu | Ala | Asp | Ser | Cys | Arg | Phe | Leu | Ser | 145 | 150 | 155 | 160 |
| Ser | Arg | Leu | Val | Met | Leu | Lys | Asn | Leu | Ala | Val | Gly | Asn | Val | Ser | Leu | 165 | 170 | 175 |     |
| Gln | Tyr | Asn | Thr | Thr | Leu | Asp | Arg | Val | Glu | Leu | Ile | Phe | Pro | Thr | Pro | 180 | 185 | 190 |     |
| Gly | Thr | Arg | Pro | Lys | Leu | Thr | Asp | Phe | Arg | Gln | Trp | Leu | Ile | Ser | Val | 195 | 200 | 205 |     |
| His | Ala | Ser | Ile | Phe | Ser | Ser | Val | Ala | Ser | Ser | Val | Thr | Leu | Phe | Ile | 210 | 215 | 220 |     |
| Val | Leu | Trp | Leu | Arg | Ile | Pro | Ala | Leu | Arg | Tyr | Val | Phe | Gly | Phe | His | 225 | 230 | 235 | 240 |
| Trp | Pro | Thr | Ala | Thr | His | His | Ser | Ser |     |     |     |     |     |     |     | 245 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad



(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|   |     |
|---|-----|
| ATG GCT CAT CAG TGT GCA CGC TTC CAT TTT TTC CTC TGT GGC TTC ATC | 48  |
| Met Ala His Gln Cys Ala Arg Phe His Phe Phe Leu Cys Gly Phe Ile |     |
| 1 5 10 15   |     |
| TGT TAC CTT GTT CAT AGT GCT TTG GCT TCG AAT TCC AGC TCT ACG CTA | 96  |
| Cys Tyr Leu Val His Ser Ala Leu Ala Ser Asn Ser Ser Ser Thr Leu |     |
| 20 25 30  |     |
| TGT TTT TGG TTT CCA TTG GCC CAC GGC AAC ACA TCA TTC GAG CTG ACC | 144 |
| Cys Phe Trp Phe Pro Leu Ala His Gly Asn Thr Ser Phe Glu Leu Thr |     |
| 35 40 45  |     |
| ATC AAC TAC ACC ATA TGC ATG CCC TGT TCT ACC AGT CAA GCG GCT CGC | 192 |
| Ile Asn Tyr Thr Ile Cys Met Pro Cys Ser Thr Ser Gln Ala Ala Arg |     |
| 50 55 60  |     |
| CAA AGG CTC GAG CCC GGT CGT AAC ATG TGG TGC AAA ATA GGG CAT GAC | 240 |
| Gln Arg Leu Glu Pro Gly Arg Asn Met Trp Cys Lys Ile Gly His Asp |     |
| 65 70 75 80   |     |
| AGG TGT GAG GAG CGT GAC CAT GAT GAG TTG TTA ATG TCC ATC CCG TCC | 288 |
| Arg Cys Glu Glu Arg Asp His Asp Glu Leu Leu Met Ser Ile Pro Ser |     |
| 85 90 95  |     |
| GGG TAC GAC AAC CTC AAA CTT GAG GGT TAT TAT GCT TGG CTG GCT TTT | 336 |
| Gly Tyr Asp Asn Leu Lys Leu Glu Gly Tyr Tyr Ala Trp Leu Ala Phe |     |
| 100 105 110   |     |
| TTG TCC TTT TCC TAC GCG GCC CAA TTC CAT CCG GAG TTG TTC GGG ATA | 384 |
| Leu Ser Phe Ser Tyr Ala Ala Gln Phe His Pro Glu Leu Phe Gly Ile |     |
| 115 120 125   |     |
| GGG AAT GTG TCG CGC GTC TTC GTG GAC AAG CGA CAC CAG TTC ATT TGT | 432 |
| Gly Asn Val Ser Arg Val Phe Val Asp Lys Arg His Gln Phe Ile Cys |     |
| 130 135 140   |     |
| GCC GAG CAT GAT GGA CAC AAT TCA ACC GTA TCT ACC GGA CAC AAC ATC | 480 |
| Ala Glu His Asp Gly His Asn Ser Thr Val Ser Thr Gly His Asn Ile |     |
| 145 150 155 160   |     |
| TCC GCA TTA TAT GCG GCA TAT TAC CAC CAC CAA ATA GAC GGG GGC AAT | 528 |
| Ser Ala Leu Tyr Ala Ala Tyr Tyr His His Gln Ile Asp Gly Gly Asn |     |
| 165 170 175   |     |

|   |     |
|---|-----|
| TGG TTC CAT TTG GAA TGG CTG CGG CCA CTC TTT TCT TCC TGG CTG GTG | 576 |
| Trp Phe His Leu Glu Trp Leu Arg Pro Leu Phe Ser Ser Trp Leu Val |     |
| 180 185 190   |     |
| CTC AAC ATA TCA TGG TTT CTG AGG CGT TCG CCT GTA AGC CCT GTT TCT | 624 |
| Leu Asn Ile Ser Trp Phe Leu Arg Arg Ser Pro Val Ser Pro Val Ser |     |
| 195 200 205   |     |
| CGA CGC ATC TAT CAG ATA TTG AGA CCA ACA CGA CCG CGG CTG CCG GTT | 672 |
| Arg Arg Ile Tyr Gln Ile Leu Arg Pro Thr Arg Pro Arg Leu Pro Val |     |
| 210 215 220   |     |
| TCA TGG TCC TTC AGG ACA TCA ATT GTT TCC GAC CTC ACG GGG TCT CAG | 720 |
| Ser Trp Ser Phe Arg Thr Ser Ile Val Ser Asp Leu Thr Gly Ser Gln |     |
| 225 230 235 240   |     |
| CAG CGC AAG AGA AAA TTT CCT TCG GAA AGT CGT CCC AAT GTC GTG AAG | 768 |
| Gln Arg Lys Arg Lys Phe Pro Ser Glu Ser Arg Pro Asn Val Val Lys |     |
| 245 250 255   |     |
| CCG TCG GTA CTC CCC AGT ACA TCA CGA TAA                         | 798 |
| Pro Ser Val Leu Pro Ser Thr Ser Arg                             |     |
| 260 265   |     |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | His | Gln | Cys | Ala | Arg | Phe | His | Phe | Phe | Leu | Cys | Gly | Phe | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Tyr | Leu | Val | His | Ser | Ala | Leu | Ala | Ser | Asn | Ser | Ser | Ser | Thr | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Phe | Trp | Phe | Pro | Leu | Ala | His | Gly | Asn | Thr | Ser | Phe | Glu | Leu | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Asn | Tyr | Thr | Ile | Cys | Met | Pro | Cys | Ser | Thr | Ser | Gln | Ala | Ala | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Arg | Leu | Glu | Pro | Gly | Arg | Asn | Met | Trp | Cys | Lys | Ile | Gly | His | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Cys | Glu | Glu | Arg | Asp | His | Asp | Glu | Leu | Leu | Met | Ser | Ile | Pro | Ser | 85  | 90  | 95  |
| Gly | Tyr | Asp | Asn | Leu | Lys | Leu | Glu | Gly | Tyr | Tyr | Ala | Trp | Leu | Ala | Phe | 100 | 105 | 110 |
| Leu | Ser | Phe | Ser | Tyr | Ala | Ala | Gln | Phe | His | Pro | Glu | Leu | Phe | Gly | Ile | 115 | 120 | 125 |
| Gly | Asn | Val | Ser | Arg | Val | Phe | Val | Asp | Lys | Arg | His | Gln | Phe | Ile | Cys | 130 | 135 | 140 |
| Ala | Glu | His | Asp | Gly | His | Asn | Ser | Thr | Val | Ser | Thr | Gly | His | Asn | Ile | 145 | 150 | 155 |
| Ser | Ala | Leu | Tyr | Ala | Ala | Tyr | Tyr | His | His | Gln | Ile | Asp | Gly | Gly | Asn | 165 | 170 | 175 |
| Trp | Phe | His | Leu | Glu | Trp | Leu | Arg | Pro | Leu | Phe | Ser | Ser | Trp | Leu | Val | 180 | 185 | 190 |
| Leu | Asn | Ile | Ser | Trp | Phe | Leu | Arg | Arg | Ser | Pro | Val | Ser | Pro | Val | Ser | 195 | 200 | 205 |
| Arg | Arg | Ile | Tyr | Gln | Ile | Leu | Arg | Pro | Thr | Arg | Pro | Arg | Leu | Pro | Val | 210 | 215 | 220 |
| Ser | Trp | Ser | Phe | Arg | Thr | Ser | Ile | Val | Ser | Asp | Leu | Thr | Gly | Ser | Gln | 225 | 230 | 235 |
| Gln | Arg | Lys | Arg | Lys | Phe | Pro | Ser | Glu | Ser | Arg | Pro | Asn | Val | Val | Lys | 245 | 250 | 255 |
| Pro | Ser | Val | Leu | Pro | Ser | Thr | Ser | Arg |     |     |     |     |     |     |     | 260 | 265 |     |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

|   |     |
|---|-----|
| ATG GCT GCG GCC ACT CTT TTC TTC CTG GCT GGT GCT CAA CAT ATC ATG | 48  |
| Met Ala Ala Ala Thr Leu Phe Phe Leu Ala Gly Ala Gln His Ile Met |     |
| 1 5 10 15   |     |
| GTT TCT GAG GCG TTC GCC TGT AAG CCC TGT TTC TCG ACG CAT CTA TCA | 96  |
| Val Ser Glu Ala Phe Ala Cys Lys Pro Cys Phe Ser Thr His Leu Ser |     |
| 20 25 30  |     |
| GAT ATT GAG ACC AAC ACG ACC GCG GCT GCC GGT TTC ATG GTC CTT CAG | 144 |
| Asp Ile Glu Thr Asn Thr Thr Ala Ala Ala Gly Phe Met Val Leu Gln |     |
| 35 40 45  |     |
| GAC ATC AAT TGT TTC CGA CCT CAC GGG GTC TCA GCA GCG CAA GAG AAA | 192 |
| Asp Ile Asn Cys Phe Arg Pro His Gly Val Ser Ala Ala Gln Glu Lys |     |
| 50 55 60  |     |
| ATT TCC TTC GGA AAG TCG TCC CAA TGT CGT GAA GCC GTC GGT ACT CCC | 240 |
| Ile Ser Phe Gly Lys Ser Ser Gln Cys Arg Glu Ala Val Gly Thr Pro |     |
| 65 70 75 80   |     |
| CAG TAC ATC ACG ATA ACG GCT AAC GTG ACC GAC GAA TCA TAC TTG TAC | 288 |
| Gln Tyr Ile Thr Ile Thr Ala Asn Val Thr Asp Glu Ser Tyr Leu Tyr |     |
| 85 90 95  |     |
| AAC GCG GAC CTG CTG ATG CTT TCT GCG TGC CTT TTC TAC GCC TCA GAA | 336 |
| Asn Ala Asp Leu Leu Met Leu Ser Ala Cys Leu Phe Tyr Ala Ser Glu |     |
| 100 105 110   |     |
| ATG AGC GAG AAA GGC TTC AAA GTC ATC TTT GGG AAT GTC TCT GGC GTT | 384 |
| Met Ser Glu Lys Gly Phe Lys Val Ile Phe Gly Asn Val Ser Gly Val |     |
| 115 120 125   |     |
| GTT TCT GCT TGT GTC AAT TTC ACA GAT TAT GTG GCC CAT GTG ACC CAA | 432 |
| Val Ser Ala Cys Val Asn Phe Thr Asp Tyr Val Ala His Val Thr Gln |     |
| 130 135 140   |     |
| CAT ACC CAG CAG CAT CAT CTG GTA ATT GAT CAC ATT CGG TTG CTG CAT | 480 |
| His Thr Gln Gln His His Leu Val Ile Asp His Ile Arg Leu Leu His |     |
| 145 150 155 160   |     |
| TTC CTG ACA CCA TCT GCA ATG AGG TGG GCT ACA ACC ATT GCT TGT TTG | 528 |
| Phe Leu Thr Pro Ser Ala Met Arg Trp Ala Thr Thr Ile Ala Cys Leu |     |
| 165 170 175   |     |
| TTC GCC ATT CTC TTG GCA ATA TGA                                 | 552 |
| Phe Ala Ile Leu Leu Ala Ile                                     |     |
| 180   |     |

